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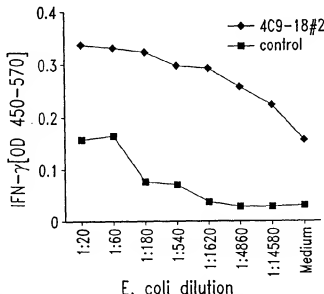
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(54) Title: COMPOUNDS AND METHODS FOR TREATMENT AND DIAGNOSIS OF CHLAMYDIAL INFECTION

(57) Abstract: Compounds and methods for the diagnosis and treatment of Chlamydial infection are disclosed. The compounds provided include polypeptides that contain at least one antigenic portion of a *Chlamydia* antigen and DNA sequences encoding such polypeptides. Pharmaceutical compositions and vaccines comprising such polypeptides or DNA sequences are also provided, together with antibodies directed against such polypeptides. Diagnostic kits containing such polypeptides or DNA sequences and a suitable detection reagent may be used for the detection of Chlamydial infection in patients and in biological samples.

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COMPOUNDS AND METHODS FOR TREATMENT AND DIAGNOSIS OF CHLAMYDIAL INFECTION

TECHNICAL FIELD

The present invention relates generally to the detection and treatment of
5 Chlamydial infection. In particular, the invention is related to polypeptides comprising
a *Chlamydia* antigen and the use of such polypeptides for the serodiagnosis and
treatment of Chlamydial infection.

BACKGROUND OF THE INVENTION

Chlamydiae are intracellular bacterial pathogens that are responsible for
10 a wide variety of important human and animal infections. *Chlamydia trachomatis* is
one of the most common causes of sexually transmitted diseases and can lead to pelvic
inflammatory disease (PID), resulting in tubal obstruction and infertility. *Chlamydia*
trachomatis may also play a role in male infertility. In 1990, the cost of treating PID in
the US was estimated to be \$4 billion. Trachoma, due to ocular infection with
15 *Chlamydia trachomatis*, is the leading cause of preventable blindness worldwide.
Chlamydia pneumonia is a major cause of acute respiratory tract infections in humans
and is also believed to play a role in the pathogenesis of atherosclerosis and, in
particular, coronary heart disease. Individuals with a high titer of antibodies to
Chlamydia pneumonia have been shown to be at least twice as likely to suffer from
20 coronary heart disease as seronegative individuals. Chlamydial infections thus
constitute a significant health problem both in the US and worldwide.

Chlamydial infection is often asymptomatic. For example, by the time a
woman seeks medical attention for PID, irreversible damage may have already occurred
resulting in infertility. There thus remains a need in the art for improved vaccines and
25 pharmaceutical compositions for the prevention and treatment of *Chlamydia* infections.
The present invention fulfills this need and further provides other related advantages.

SUMMARY OF THE INVENTION

The present invention provides compositions and methods for the
diagnosis and therapy of *Chlamydia* infection. In one aspect, the present invention
30 provides polypeptides comprising an immunogenic portion of a *Chlamydia* antigen, or a
variant of such an antigen. Certain portions and other variants are immunogenic, such
that the ability of the variant to react with antigen-specific antisera is not substantially
diminished. Within certain embodiments, the polypeptide comprises an amino acid

sequence encoded by a polynucleotide sequence selected from the group consisting of (a) a sequence of SEQ ID NO: 1, 15, 21-25, 44-64, 66-76, 79-88, 110-119, 120, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-290; (b) the complements of said sequences; and (c) sequences that hybridize to a sequence of (a) or (b) under moderately stringent conditions. In specific embodiments, the polypeptides of the present invention comprise at least a portion of a *Chlamydial* protein that includes an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO: 5-14, 17-20, 26, 28, 30-32, 34, 39-43, 65, 89-109, 138-158, 167, 168, 224-262, 246, 247, 254-256, 292, 294-305 and variants thereof.

10 The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least 15 amino acid residues of a *Chlamydial* protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

15 In a related aspect, polynucleotide sequences encoding the above polypeptides, recombinant expression vectors comprising one or more of these polynucleotide sequences and host cells transformed or transfected with such expression vectors are also provided.

20 In another aspect, the present invention provides fusion proteins comprising an inventive polypeptide, or, alternatively, an inventive polypeptide and a known *Chlamydia* antigen, as well as polynucleotides encoding such fusion proteins, in combination with a physiologically acceptable carrier or immunostimulant for use as pharmaceutical compositions and vaccines thereof.

25 The present invention further provides pharmaceutical compositions that comprise: (a) an antibody, both polyclonal and monoclonal, or antigen-binding fragment thereof that specifically binds to a *Chlamydial* protein; and (b) a physiologically acceptable carrier. Within other aspects, the present invention provides pharmaceutical compositions that comprise one or more *Chlamydia* polypeptides disclosed herein, or a polynucleotide molecule encoding such a polypeptide, and a physiologically acceptable carrier. The invention also provides vaccines for 30 prophylactic and therapeutic purposes comprising one or more of the disclosed polypeptides and an immunostimulant, as defined herein, together with vaccines comprising one or more polynucleotide sequences encoding such polypeptides and an immunostimulant.

35 In yet another aspect, methods are provided for inducing protective immunity in a patient, comprising administering to a patient an effective amount of one or more of the above pharmaceutical compositions or vaccines.

In yet a further aspect, methods for the treatment of *Chlamydia* infection in a patient are provided, the methods comprising obtaining peripheral blood mononuclear cells (PBMC) from the patient, incubating the PBMC with a polypeptide of the present invention (or a polynucleotide that encodes such a polypeptide) to provide incubated T cells and administering the incubated T cells to the patient. The present invention additionally provides methods for the treatment of *Chlamydia* infection that comprise incubating antigen presenting cells with a polypeptide of the present invention (or a polynucleotide that encodes such a polypeptide) to provide incubated antigen presenting cells and administering the incubated antigen presenting cells to the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient. In certain embodiments, the antigen presenting cells are selected from the group consisting of dendritic cells, macrophages, monocytes, B-cells, and fibroblasts. Compositions for the treatment of *Chlamydia* infection comprising T cells or antigen presenting cells that have been incubated with a polypeptide or polynucleotide of the present invention are also provided. Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

The present invention further provides, within other aspects, methods for removing *Chlamydial*-infected cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a *Chlamydial* protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of *Chlamydial* infection in a patient, comprising administering to a patient a biological sample treated as described above. In further aspects of the subject invention, methods and diagnostic kits are provided for detecting *Chlamydia* infection in a patient. In one embodiment, the method comprises: (a) contacting a biological sample with at least one of the polypeptides or fusion proteins disclosed herein; and (b) detecting in the sample the presence of binding agents that bind to the polypeptide or fusion protein, thereby detecting *Chlamydia* infection in the biological sample. Suitable biological samples include whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid and urine. In one embodiment, the diagnostic kits comprise one or more of the polypeptides or fusion proteins disclosed herein in combination with a detection reagent. In yet another embodiment, the diagnostic kits comprise either a monoclonal antibody or a polyclonal antibody that binds with a polypeptide of the present invention.

The present invention also provides methods for detecting *Chlamydia* infection comprising: (a) obtaining a biological sample from a patient; (b) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, at least one of the oligonucleotide primers being specific for a polynucleotide sequence disclosed herein; and (c) detecting in the sample a polynucleotide sequence that amplifies in the presence of the oligonucleotide primers. In one embodiment, the oligonucleotide primer comprises at least about 10 contiguous nucleotides of a polynucleotide sequence peptide disclosed herein, or of a sequence that hybridizes thereto.

In a further aspect, the present invention provides a method for detecting *Chlamydia* infection in a patient comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with an oligonucleotide probe specific for a polynucleotide sequence disclosed herein; and (c) detecting in the sample a polynucleotide sequence that hybridizes to the oligonucleotide probe. In one embodiment, the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a polynucleotide sequence disclosed herein, or a sequence that hybridizes thereto.

These and other aspects of the present invention will become apparent upon reference to the following detailed description. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

SEQUENCE IDENTIFIERS

SEQ ID NO: 1 is the determined DNA sequence for the *C. trachomatis* clone 1-B1-66.

SEQ ID NO: 2 is the determined DNA sequence for the *C. trachomatis* clone 4-D7-28.

SEQ ID NO: 3 is the determined DNA sequence for the *C. trachomatis* clone 3-G3-10.

SEQ ID NO: 4 is the determined DNA sequence for the *C. trachomatis* clone 10-C10-31.

SEQ ID NO: 5 is the predicted amino acid sequence for 1-B1-66.

SEQ ID NO: 6 is the predicted amino acid sequence for 4-D7-28.

SEQ ID NO: 7 is a first predicted amino acid sequence for 3-G3-10.

SEQ ID NO: 8 is a second predicted amino acid sequence for 3-G3-10.

SEQ ID NO: 9 is a third predicted amino acid sequence for 3-G3-10.

- SEQ ID NO: 10 is a fourth predicted amino acid sequence for 3-G3-10.
SEQ ID NO: 11 is a fifth predicted amino acid sequence for 3-G3-10.
SEQ ID NO: 12 is the predicted amino acid sequence for 10-C10-31.
SEQ ID NO: 13 is the amino acid sequence of the synthetic peptide 1-
5 B1-66/48-67.
SEQ ID NO: 14 is the amino acid sequence of the synthetic peptide 1-
B1-66/58-77.
SEQ ID NO: 15 is the determined DNA sequence for the *C. trachomatis*
serovar LGV II clone 2C7-8
10 SEQ ID NO: 16 is a DNA sequence of a putative open reading frame
from a region of the *C. trachomatis* serovar D genome to which 2C7-8 maps
SEQ ID NO: 17 is the predicted amino acid sequence encoded by the
DNA sequence of SEQ ID NO: 16
SEQ ID NO: 18 is the amino acid sequence of the synthetic peptide
15 CtC7.8-12
SEQ ID NO: 19 is the amino acid sequence of the synthetic peptide
CtC7.8-13
SEQ ID NO: 20 is the predicted amino acid sequence encoded by a
second putative open reading from *C. trachomatis* serovar D
20 SEQ ID NO: 21 is the determined DNA sequence for clone 4C9-18 from
C. trachomatis LGV II
SEQ ID NO: 22 is the determined DNA sequence homologous to
Lipoamide Dehydrogenase from *C. trachomatis* LGV II
SEQ ID NO: 23 is the determined DNA sequence homologous to
25 Hypothetical protein from *C. trachomatis* LGV II
SEQ ID NO: 24 is the determined DNA sequence homologous to
Ubiquinone Methyltransferase from *C. trachomatis* LGV II
SEQ ID NO: 25 is the determined DNA sequence for clone 4C9-18#2
BL21 pLysS from *C. trachomatis* LGV II
30 SEQ ID NO: 26 is the predicted amino acid sequence for 4C9-18#2 from
C. trachomatis LGV II
SEQ ID NO: 27 is the determined DNA sequence for Cp-SWIB from *C.*
pneumonia strain TWAR
SEQ ID NO: 28 is the predicted amino acid sequence for Cp-SWIB from
35 *C. pneumonia* strain TWAR

SEQ ID NO: 29 is the determined DNA sequence for Cp-S13 from *C. pneumonia* strain TWAR

SEQ ID NO: 30 is the predicted amino acid sequence for Cp-S13 from *C. pneumonia* strain TWAR

5 SEQ ID NO: 31 is the amino acid sequence for a 10mer consensus peptide from CtC7.8-12 and CtC7.8-13

SEQ ID NO: 32 is the predicted amino acid sequence for clone 2C7-8 from *C. trachomatis* LGV II

10 SEQ ID NO: 33 is the DNA sequence corresponding to nucleotides 597304-597145 of the *C. trachomatis* serovar D genome (NCBI, BLASTN search), which shows homology to clone 2C7-8

SEQ ID NO: 34 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 33

15 SEQ ID NO: 35 is the DNA sequence for C.p. SWIB Nde (5' primer) from *C. pneumonia*

SEQ ID NO: 36 is the DNA sequence for C.p. SWIB EcoRI (3' primer) from *C. pneumonia*

SEQ ID NO : 37 is the DNA sequence for C.p. S13 Nde (5' primer) from *C. pneumonia*

20 SEQ ID NO: 38 is the DNA sequence for C.p. S13 EcoRI (3' primer) from *C. pneumonia*

SEQ ID NO: 39 is the amino acid sequence for CtSwib 52-67 peptide from *C. trachomatis* LGV II

25 SEQ ID NO: 40 is the amino acid sequence for CpSwib 53-68 peptide from *C. pneumonia*

SEQ ID NO: 41 is the amino acid sequence for HuSwib 288-302 peptide from Human SWI domain

SEQ ID NO: 42 is the amino acid sequence for CtSWI-T 822-837 peptide from the topoisomerase-SWIB fusion of *C. trachomatis*

30 SEQ ID NO: 43 is the amino acid sequence for CpSWI-T 828-842 peptide from the topoisomerase-SWIB fusion of *C. pneumonia*

SEQ ID NO: 44 is a first determined DNA sequence for the *C. trachomatis* LGV II clone 19783.3.jen.seq(1>509)CTL2#11-3', representing the 3' end.

35 SEQ ID NO: 45 is a second determined DNA sequence for the *C. trachomatis* LGV II clone 19783.4.jen.seq(1>481)CTL2#11-5', representing the 5' end.

SEQ ID NO: 46 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19784CTL2_12consensus.seq(1>427)CTL2#12.

SEQ ID NO: 47 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19785.4.jen.seq(1>600)CTL2#16-5', representing the 5' end.

- 5 SEQ ID NO: 48 is a first determined DNA sequence for the *C. trachomatis* LGV II clone 19786.3.jen.seq(1>600)CTL2#18-3', representing the 3' end.

SEQ ID NO: 49 is a second determined DNA sequence for the *C. trachomatis* LGV II clone 19786.4.jen.seq(1>600)CTL2#18-5', representing the 5' end.

- 10 SEQ ID NO: 50 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19788CTL2_21consensus.seq(1>406)CTL2#21.

SEQ ID NO: 51 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19790CTL2_23consensus.seq(1>602)CTL2#23.

SEQ ID NO: 52 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19791CTL2_24consensus.seq(1>145)CTL2#24.

- 15 SEQ ID NO: 53 is the determined DNA sequence for the *C. trachomatis* LGV II clone CTL2#4.

SEQ ID NO: 54 is the determined DNA sequence for the *C. trachomatis* LGV II clone CTL2#8b.

- 20 SEQ ID NO: 55 is the determined DNA sequence for the *C. trachomatis* LGV II clone 15-G1-89, sharing homology to the lipoamide dehydrogenase gene CT557.

SEQ ID NO: 56 is the determined DNA sequence for the *C. trachomatis* LGV II clone 14-H1-4, sharing homology to the thiol specific antioxidant gene CT603.

- 25 SEQ ID NO: 57 is the determined DNA sequence for the *C. trachomatis* LGV II clone 12-G3-83, sharing homology to the hypothetical protein CT622.

SEQ ID NO: 58 is the determined DNA sequence for the *C. trachomatis* LGV II clone 12-B3-95, sharing homology to the lipoamide dehydrogenase gene CT557.

- 30 SEQ ID NO: 59 is the determined DNA sequence for the *C. trachomatis* LGV II clone 11-H4-28, sharing homology to the dnaK gene CT396.

SEQ ID NO: 60 is the determined DNA sequence for the *C. trachomatis* LGV II clone 11-H3-68, sharing partial homology to the PGP6-D virulence protein and L1 ribosomal gene CT318.

- 35 SEQ ID NO: 61 is the determined DNA sequence for the *C. trachomatis* LGV II clone 11-G1-34, sharing partial homology to the malate dehydrogenase gene CT376 and to the glycogen hydrolase gene CT042.

SEQ ID NO: 62 is the determined DNA sequence for the *C. trachomatis* LGV II clone 11-G10-46, sharing homology to the hypothetical protein CT610.

SEQ ID NO: 63 is the determined DNA sequence for the *C. trachomatis* LGV II clone 11-C12-91, sharing homology to the OMP2 gene CT443.

- 5 SEQ ID NO: 64 is the determined DNA sequence for the *C. trachomatis* LGV II clone 11-A3-93, sharing homology to the HAD superfamily gene CT103.

SEQ ID NO: 65 is the determined amino acid sequence for the *C. trachomatis* LGV II clone 14-H1-4, sharing homology to the thiol specific antioxidant gene CT603.

- 10 SEQ ID NO: 66 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#9.

SEQ ID NO: 67 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#7.

- 15 SEQ ID NO: 68 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#6.

SEQ ID NO: 69 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#5.

SEQ ID NO: 70 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#2.

- 20 SEQ ID NO: 71 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#1.

SEQ ID NO: 72 is a first determined DNA sequence for the *C. trachomatis* LGV II clone 23509.2CtL2#3-5', representing the 5' end.

- 25 SEQ ID NO: 73 is a second determined DNA sequence for the *C. trachomatis* LGV II clone 23509.1CtL2#3-3', representing the 3' end.

SEQ ID NO: 74 is a first determined DNA sequence for the *C. trachomatis* LGV II clone 22121.2CtL2#10-5', representing the 5' end.

SEQ ID NO: 75 is a second determined DNA sequence for the *C. trachomatis* LGV II clone 22121.1CtL2#10-3', representing the 3' end.

- 30 SEQ ID NO: 76 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19787.6CtL2#19-5', representing the 5' end.

SEQ ID NO: 77 is the determined DNA sequence for the *C. pneumoniae* LGV II clone CpS13-His.

- 35 SEQ ID NO: 78 is the determined DNA sequence for the *C. pneumoniae* LGV II clone Cp_SWIB-His.

SEQ ID NO: 79 is the determined DNA sequence for the *C. trachomatis* LGV II clone 23-G7-68, sharing partial homology to the L11, L10 and L1 ribosomal protein.

- 5 SEQ ID NO: 80 is the determined DNA sequence for the *C. trachomatis* LGV II clone 22-F8-91, sharing homology to the pmpC gene.

SEQ ID NO: 81 is the determined DNA sequence for the *C. trachomatis* LGV II clone 21-E8-95, sharing homology to the CT610-CT613 genes.

SEQ ID NO: 82 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19-F12-57, sharing homology to the CT858 and recA genes.

- 10 SEQ ID NO: 83 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19-F12-53, sharing homology to the CT445 gene encoding glutamyl tRNA synthetase.

SEQ ID NO: 84 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19-A5-54, sharing homology to the cryptic plasmid gene.

- 15 SEQ ID NO: 85 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-E11-72, sharing partial homology to the OppC_2 and pmpD genes.

SEQ ID NO: 86 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-C1-77, sharing partial homology to the CT857 and CT858 open reading frames.

- 20 SEQ ID NO: 87 is the determined DNA sequence for the *C. trachomatis* LGV II clone 15-H2-76, sharing partial homology to the pmpD and SycE genes, and to the CT089 ORF.

SEQ ID NO: 88 is the determined DNA sequence for the *C. trachomatis* LGV II clone 15-A3-26, sharing homology to the CT858 ORF.

- 25 SEQ ID NO: 89 is the determined amino acid sequence for the *C. pneumoniae* clone Cp_SWIB-His.

SEQ ID NO: 90 is the determined amino acid sequence for the *C. trachomatis* LGV II clone CtL2_LPDA_FL.

- 30 *pneumoniae* clone CpS13-His.

SEQ ID NO: 91 is the determined amino acid sequence for the *C. trachomatis* LGV II clone CtL2_TSA_FL.

SEQ ID NO: 92 is the determined amino acid sequence for the *C. trachomatis* LGV II clone CtL2_TSA_FL.

- 35 SEQ ID NO: 93 is the amino acid sequence for Ct-Swib 43-61 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 94 is the amino acid sequence for Ct-Swib 48-67 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 95 is the amino acid sequence for Ct-Swib 52-71 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 96 is the amino acid sequence for Ct-Swib 58-77 peptide from *C. trachomatis* LGV II.

5 SEQ ID NO: 97 is the amino acid sequence for Ct-Swib 63-82 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 98 is the amino acid sequence for Ct-Swib 51-66 peptide from *C. trachomatis* LGV II.

10 SEQ ID NO: 99 is the amino acid sequence for Cp-Swib 52-67 peptide from *C. pneumonia*.

SEQ ID NO: 100 is the amino acid sequence for Cp-Swib 37-51 peptide from *C. pneumonia*.

SEQ ID NO: 101 is the amino acid sequence for Cp-Swib 32-51 peptide from *C. pneumonia*.

15 SEQ ID NO: 102 is the amino acid sequence for Cp-Swib 37-56 peptide from *C. pneumonia*.

SEQ ID NO: 103 is the amino acid sequence for Ct-Swib 36-50 peptide from *C. trachomatis*.

20 SEQ ID NO: 104 is the amino acid sequence for Ct-S13 46-65 peptide from *C. trachomatis*.

SEQ ID NO: 105 is the amino acid sequence for Ct-S13 60-80 peptide from *C. trachomatis*.

SEQ ID NO: 106 is the amino acid sequence for Ct-S13 1-20 peptide from *C. trachomatis*.

25 SEQ ID NO: 107 is the amino acid sequence for Ct-S13 46-65 peptide from *C. trachomatis*.

SEQ ID NO: 108 is the amino acid sequence for Ct-S13 56-75 peptide from *C. trachomatis*.

30 SEQ ID NO: 109 is the amino acid sequence for Cp-S13 56-75 peptide from *C. pneumoniae*.

SEQ ID NO: 110 is the determined DNA sequence for the *C. trachomatis* LGV II clone 21-G12-60, containing partial open reading frames for hypothetical proteins CT875, CT229 and CT228.

35 SEQ ID NO: 111 is the determined DNA sequence for the *C. trachomatis* LGV II clone 22-B3-53, sharing homology to the CT110 ORF of GroEL.

SEQ ID NO: 112 is the determined DNA sequence for the *C. trachomatis* LGV II clone 22-A1-49, sharing partial homology to the CT660 and CT659 ORFs.

5 SEQ ID NO: 113 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-E2-9, sharing partial homology to the CT611 and CT 610 ORFs.

SEQ ID NO: 114 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-C10-31, sharing partial homology to the CT858 ORF.

10 SEQ ID NO: 115 is the determined DNA sequence for the *C. trachomatis* LGV II clone 21-C7-66, sharing homology to the dnaK-like gene.

SEQ ID NO: 116 is the determined DNA sequence for the *C. trachomatis* LGV II clone 20-G3-45, containing part of the pmpB gene CT413.

SEQ ID NO: 117 is the determined DNA sequence for the *C. trachomatis* LGV II clone 18-C5-2, sharing homology to the S1 ribosomal protein ORF.

15 SEQ ID NO: 118 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-C5-19, containing part of the ORFs for CT431 and CT430.

20 SEQ ID NO: 119 is the determined DNA sequence for the *C. trachomatis* LGV II clone 16-D4-22, contains partial sequences of ORF3 and ORF4 of the plasmid for growth within mammalian cells.

SEQ ID NO: 120 is the determined full-length DNA sequence for the *C. trachomatis* serovar LGV II Cap1 gene CT529.

SEQ ID NO: 121 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar LGV II Cap1 gene CT529.

25 SEQ ID NO: 122 is the determined full-length DNA sequence for the *C. trachomatis* serovar E Cap1 gene CT529.

SEQ ID NO: 123 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar E Cap1 gene CT529.

30 SEQ ID NO: 124 is the determined full-length DNA sequence for the *C. trachomatis* serovar 1A Cap1 gene CT529.

SEQ ID NO: 125 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar 1A Cap1 gene CT529.

SEQ ID NO: 126 is the determined full-length DNA sequence for the *C. trachomatis* serovar G Cap1 gene CT529.

35 SEQ ID NO: 127 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar G Cap1 gene CT529.

- SEQ ID NO: 128 is the determined full-length DNA sequence for the *C. trachomatis* serovar F1 NII Cap1 gene CT529.
- SEQ ID NO: 129 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar F1 NII Cap1 gene CT529.
- 5 SEQ ID NO: 130 is the determined full-length DNA sequence for the *C. trachomatis* serovar L1 Cap1 gene CT529.
- SEQ ID NO: 131 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar L1 Cap1 gene CT529.
- SEQ ID NO: 132 is the determined full-length DNA sequence for the *C. trachomatis* serovar L3 Cap1 gene CT529.
- 10 SEQ ID NO: 133 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar L3 Cap1 gene CT529.
- SEQ ID NO: 134 is the determined full-length DNA sequence for the *C. trachomatis* serovar Ba Cap1 gene CT529.
- 15 SEQ ID NO: 135 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar Ba Cap1 gene CT529.
- SEQ ID NO: 136 is the determined full-length DNA sequence for the *C. trachomatis* serovar MOPN Cap1 gene CT529.
- SEQ ID NO: 137 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar MOPN Cap1 gene CT529.
- 20 SEQ ID NO: 138 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #124-139 of *C. trachomatis* serovar L2.
- SEQ ID NO: 139 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #132-147 of *C. trachomatis* serovar L2.
- 25 SEQ ID NO: 140 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #138-155 of *C. trachomatis* serovar L2.
- SEQ ID NO: 141 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #146-163 of *C. trachomatis* serovar L2.
- SEQ ID NO: 142 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #154-171 of *C. trachomatis* serovar L2.
- 30 SEQ ID NO: 143 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #162-178 of *C. trachomatis* serovar L2.
- SEQ ID NO: 144 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #138-147 of *C. trachomatis* serovar L2.
- 35 SEQ ID NO: 145 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #139-147 of *C. trachomatis* serovar L2.

- SEQ ID NO: 146 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #140-147 of *C. trachomatis* serovar L2.
- SEQ ID NO: 147 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #138-146 of *C. trachomatis* serovar L2.
- 5 SEQ ID NO: 148 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #138-145 of *C. trachomatis* serovar L2.
- SEQ ID NO: 149 is the determined amino acid sequence for the Cap1 CT529 ORF peptide # F140->I of *C. trachomatis* serovar L2.
- SEQ ID NO: 150 is the determined amino acid sequence for the Cap1
- 10 CT529 ORF peptide # #S139>Ga of *C. trachomatis* serovar L2.
- SEQ ID NO: 151 is the determined amino acid sequence for the Cap1 CT529 ORF peptide # #S139>Gb of *C. trachomatis* serovar L2.
- SEQ ID NO: 152 is the determined amino acid sequence for the peptide # 2 C7.8-6 of the 216aa ORF of *C. trachomatis* serovar L2.
- 15 SEQ ID NO: 153 is the determined amino acid sequence for the peptide # 2 C7.8-7 of the 216aa ORF of *C. trachomatis* serovar L2.
- SEQ ID NO: 154 is the determined amino acid sequence for the peptide # 2 C7.8-8 of the 216aa ORF of *C. trachomatis* serovar L2.
- SEQ ID NO: 155 is the determined amino acid sequence for the peptide
- 20 # 2 C7.8-9 of the 216aa ORF of *C. trachomatis* serovar L2.
- SEQ ID NO: 156 is the determined amino acid sequence for the peptide # 2 C7.8-10 of the 216aa ORF of *C. trachomatis* serovar L2.
- SEQ ID NO: 157 is the determined amino acid sequence for the 53 amino acid residue peptide of the 216aa ORF within clone 2C7.8 of *C. trachomatis*
- 25 serovar L2.
- SEQ ID NO: 158 is the determined amino acid sequence for the 52 amino acid residue peptide of the CT529 ORF within clone 2C7.8 of *C. trachomatis* serovar L2.
- SEQ ID NO: 159 is the determined DNA sequence for the 5' (forward)
- 30 primer for cloning full-length CT529 serovar L2.
- SEQ ID NO: 160 is the determined DNA sequence for the 5' (reverse) primer for cloning full-length CT529 serovar L2.
- SEQ ID NO: 161 is the determined DNA sequence for the 5' (forward) primer for cloning full-length CT529 for serovars other than L2 and MOPN.
- 35 SEQ ID NO: 162 is the determined DNA sequence for the 5' (reverse) primer for cloning full-length CT529 serovars other than L2 and MOPN.

- SEQ ID NO: 163 is the determined DNA sequence for the 5' (forward) primer for cloning full-length CT529 serovar MOPN.
- SEQ ID NO: 164 is the determined DNA sequence for the 5' (reverse) primer for cloning full-length CT529 serovar MOPN.
- 5 SEQ ID NO: 165 is the determined DNA sequence for the 5' (forward) primer for pBIB-KS.
- SEQ ID NO: 166 is the determined DNA sequence for the 5' (reverse) primer for pBIB-KS.
- SEQ ID NO: 167 is the determined amino acid sequence for the 9-mer epitope peptide Cap1#139-147 from serovar L2.
- 10 SEQ ID NO: 168 is the determined amino acid sequence for the 9-mer epitope peptide Cap1#139-147 from serovar D.
- SEQ ID NO: 169 is the determined full-length DNA sequence for the *C. trachomatis* pmpI gene.
- 15 SEQ ID NO: 170 is the determined full-length DNA sequence for the *C. trachomatis* pmpG gene.
- SEQ ID NO: 171 is the determined full-length DNA sequence for the *C. trachomatis* pmpE gene.
- SEQ ID NO: 172 is the determined full-length DNA sequence for the *C. trachomatis* pmpD gene.
- 20 SEQ ID NO: 173 is the determined full-length DNA sequence for the *C. trachomatis* pmpC gene.
- SEQ ID NO: 174 is the determined full-length DNA sequence for the *C. trachomatis* pmpB gene.
- 25 SEQ ID NO: 175 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpI gene.
- SEQ ID NO: 176 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpG gene.
- SEQ ID NO: 177 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpE gene.
- 30 SEQ ID NO: 178 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpD gene.
- SEQ ID NO: 179 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpC gene.
- 35 SEQ ID NO: 180 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpB gene.

SEQ ID NO: 181 is the determined DNA sequence minus the signal sequence for the *C. trachomatis* pmpI gene.

SEQ ID NO: 182 is a subsequently determined full-length DNA sequence for the *C. trachomatis* pmpG gene.

5 SEQ ID NO: 183 is the determined DNA sequence minus the signal sequence for the *C. trachomatis* pmpE gene.

SEQ ID NO: 184 is a first determined DNA sequence representing the carboxy terminus for the *C. trachomatis* pmpD gene.

10 SEQ ID NO: 185 is a second determined DNA sequence representing the amino terminus minus the signal sequence for the *C. trachomatis* pmpD gene.

SEQ ID NO: 186 is a first determined DNA sequence representing the carboxy terminus for the *C. trachomatis* pmpC gene.

SEQ ID NO: 187 is a second determined DNA sequence representing the amino terminus minus the signal sequence for the *C. trachomatis* pmpC gene.

15 SEQ ID NO: 188 is the determined DNA sequence representing the *C. pneumoniae* serovar MOMPS pmp gene in a fusion molecule with Ra12.

SEQ ID NO: 189 is the predicted amino acid sequence minus the signal sequence for the *C. trachomatis* pmpI gene.

20 SEQ ID NO: 190 is subsequently predicted amino acid sequence for the *C. trachomatis* pmpG gene.

SEQ ID NO: 191 is the predicted amino acid sequence minus the signal sequence for the *C. trachomatis* pmpE gene.

SEQ ID NO: 192 is a first predicted amino acid sequence representing the carboxy terminus for the *C. trachomatis* pmpD gene.

25 SEQ ID NO: 193 is a second predicted amino acid sequence representing the Amino terminus minus the signal sequence for the *C. trachomatis* pmpD gene.

SEQ ID NO: 194 is a first predicted amino acid sequence representing the Carboxy terminus for the *C. trachomatis* pmpC gene.

30 SEQ ID NO: 195 is a second predicted amino acid sequence representing the Amino terminus for the *C. trachomatis* pmpC gene.

SEQ ID NO: 196 is the predicted amino acid sequence representing the *C. pneumoniae* serovar MOMPS pmp gene in a fusion molecule with Ra12.

SEQ ID NO: 197 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpC gene in the SKB vaccine vector.

35 SEQ ID NO: 198 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpC gene in the SKB vaccine vector.

SEQ ID NO: 199 is the determined DNA sequence for the insertion sequence for cloning the *C. trachomatis* pmpC gene in the SKB vaccine vector.

SEQ ID NO: 200 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpD gene in the SKB vaccine vector.

5 SEQ ID NO: 201 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpD gene in the SKB vaccine vector.

SEQ ID NO: 202 is the determined DNA sequence for the insertion sequence for cloning the *C. trachomatis* pmpD gene in the SKB vaccine vector.

10 SEQ ID NO: 203 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpE gene in the SKB vaccine vector.

SEQ ID NO: 204 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpE gene in the SKB vaccine vector.

SEQ ID NO: 205 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpG gene in the SKB vaccine vector.

15 SEQ ID NO: 206 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpG gene in the SKB vaccine vector.

SEQ ID NO: 207 is the determined DNA sequence for the 5' oligo primer for cloning the amino terminus portion of the *C. trachomatis* pmpC gene in the pET17b vector.

20 SEQ ID NO: 208 is the determined DNA sequence for the 3' oligo primer for cloning the amino terminus portion of the *C. trachomatis* pmpC gene in the pET17b vector.

SEQ ID NO: 209 is the determined DNA sequence for the 5' oligo primer for cloning the carboxy terminus portion of the *C. trachomatis* pmpC gene in the pET17b vector.

25 SEQ ID NO: 210 is the determined DNA sequence for the 3' oligo primer for cloning the carboxy terminus portion of the *C. trachomatis* pmpC gene in the pET17b vector.

SEQ ID NO: 211 is the determined DNA sequence for the 5' oligo primer for cloning the amino terminus portion of the *C. trachomatis* pmpD gene in the pET17b vector.

30 SEQ ID NO: 212 is the determined DNA sequence for the 3' oligo primer for cloning the amino terminus portion of the *C. trachomatis* pmpD gene in the pET17b vector.

SEQ ID NO: 213 is the determined DNA sequence for the 5' oligo primer for cloning the carboxy terminus portion of the *C. trachomatis* pmpD gene in the pET17b vector.

5 SEQ ID NO: 214 is the determined DNA sequence for the 3' oligo primer for cloning the carboxy terminus portion of the *C. trachomatis* pmpD gene in the pET17b vector.

SEQ ID NO: 215 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpE gene in the pET17b vector.

10 SEQ ID NO: 216 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpE gene in the pET17b vector.

SEQ ID NO: 217 is the determined DNA sequence for the insertion sequence for cloning the *C. trachomatis* pmpE gene in the pET17b vector.

SEQ ID NO: 218 is the amino acid sequence for the insertion sequence for cloning the *C. trachomatis* pmpE gene in the pET17b vector.

15 SEQ ID NO: 219 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpG gene in the pET17b vector.

SEQ ID NO: 220 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpG gene in the pET17b vector.

20 SEQ ID NO: 221 is the amino acid sequence for the insertion sequence for cloning the *C. trachomatis* pmpG gene in the pET17b vector.

SEQ ID NO: 222 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpl gene in the pET17b vector.

SEQ ID NO: 223 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpl gene in the pET17b vector.

25 SEQ ID NO: 224 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 1-20.

SEQ ID NO: 225 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 6-25.

30 SEQ ID NO: 226 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 12-31.

SEQ ID NO: 227 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 17-36.

SEQ ID NO: 228 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 22-41.

35 SEQ ID NO: 229 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 27-46.

- SEQ ID NO: 230 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 42-61.
- SEQ ID NO: 231 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 46-65.
- 5 SEQ ID NO: 232 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 51-70.
- SEQ ID NO: 233 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 56-75.
- 10 SEQ ID NO: 234 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 61-80.
- SEQ ID NO: 235 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 66-87.
- SEQ ID NO: 236 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 103-122.
- 15 SEQ ID NO: 237 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 108-127.
- SEQ ID NO: 238 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 113-132.
- 20 SEQ ID NO: 239 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 118-137.
- SEQ ID NO: 240 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 123-143.
- SEQ ID NO: 241 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 128-147.
- 25 SEQ ID NO: 242 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 133-152.
- SEQ ID NO: 243 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 137-156.
- 30 SEQ ID NO: 244 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 142-161.
- SEQ ID NO: 245 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 147-166.
- SEQ ID NO: 246 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 152-171.
- 35 SEQ ID NO: 247 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 157-176.

- SEQ ID NO: 248 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 162-181.
- SEQ ID NO: 249 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 167-186.
- 5 SEQ ID NO: 250 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 171-190.
- SEQ ID NO: 251 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 171-186.
- 10 SEQ ID NO: 252 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 175-186.
- SEQ ID NO: 252 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 175-186.
- SEQ ID NO: 253 is the determined amino acid sequence for the *C. pneumoniae* OMCB peptide 185-198.
- 15 SEQ ID NO: 254 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 96-115.
- SEQ ID NO: 255 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 101-120.
- 20 SEQ ID NO: 256 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 106-125.
- SEQ ID NO: 257 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 111-130.
- SEQ ID NO: 258 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 116-135.
- 25 SEQ ID NO: 259 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 121-140.
- SEQ ID NO: 260 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 126-145.
- SEQ ID NO: 261 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 131-150.
- 30 SEQ ID NO: 262 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 136-155.
- SEQ ID NO: 263 is the determined full-length DNA sequence for the *C. trachomatis* CT529/Cap 1 gene serovar I.
- 35 SEQ ID NO: 264 is the predicted full-length amino sequence for the *C. trachomatis* CT529/Cap 1 gene serovar I.

SEQ ID NO: 265 is the determined full-length DNA sequence for the *C. trachomatis* CT529/Cap 1 gene serovar K.

SEQ ID NO: 266 is the predicted full-length amino sequence for the *C. trachomatis* CT529/Cap 1 gene serovar K.

- 5 SEQ ID NO: 267 is the determined DNA sequence for the *C. trachomatis* clone 17-G4-36 sharing homology to part of the ORF of DNA-directed RNA polymerase beta subunit- CT315 in serD.

SEQ ID NO: 268 is the determined DNA sequence for the partial sequence of the *C. trachomatis* CT016 gene in clone 2E10.

- 10 SEQ ID NO: 269 is the determined DNA sequence for the partial sequence of the *C. trachomatis* tRNA synthase gene in clone 2E10.

SEQ ID NO: 270 is the determined DNA sequence for the partial sequence for the *C. trachomatis* clpX gene in clone 2E10.

- 15 SEQ ID NO: 271 is a first determined DNA sequence for the *C. trachomatis* clone Ctl2gam-30 representing the 5' end.

SEQ ID NO: 272 is a second determined DNA sequence for the *C. trachomatis* clone Ctl2gam-30 representing the 3' end.

SEQ ID NO: 273 is the determined DNA sequence for the *C. trachomatis* clone Ctl2gam-28.

- 20 SEQ ID NO: 274 is the determined DNA sequence for the *C. trachomatis* clone Ctl2gam-27.

SEQ ID NO: 275 is the determined DNA sequence for the *C. trachomatis* clone Ctl2gam-26.

- 25 SEQ ID NO: 276 is the determined DNA sequence for the *C. trachomatis* clone Ctl2gam-24.

SEQ ID NO: 277 is the determined DNA sequence for the *C. trachomatis* clone Ctl2gam-23.

SEQ ID NO: 278 is the determined DNA sequence for the *C. trachomatis* clone Ctl2gam-21.

- 30 SEQ ID NO: 279 is the determined DNA sequence for the *C. trachomatis* clone Ctl2gam-18.

SEQ ID NO: 280 is the determined DNA sequence for the *C. trachomatis* clone Ctl2gam-17.

- 35 SEQ ID NO: 281 is a first determined DNA sequence for the *C. trachomatis* clone Ctl2gam-15 representing the 5' end.

SEQ ID NO: 282 is a second determined DNA sequence for the *C. trachomatis* clone CtL2gam-15 representing the 3' end.

SEQ ID NO: 283 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-13.

5 SEQ ID NO: 284 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-10.

SEQ ID NO: 285 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-8.

10 SEQ ID NO: 286 is a first determined DNA sequence for the *C. trachomatis* clone CtL2gam-6 representing the 5' end.

SEQ ID NO: 287 is a second determined DNA sequence for the *C. trachomatis* clone CtL2gam-6 representing the 3' end.

SEQ ID NO: 288 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-5.

15 SEQ ID NO: 289 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-2.

SEQ ID NO: 290 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-1.

20 SEQ ID NO: 291 is the determined full-length DNA sequence for the *C. pneumoniae* homologue of the CT529 gene.

SEQ ID NO: 292 is the predicted full-length amino acid sequence for the *C. pneumoniae* homologue of the CT529 gene.

SEQ ID NO: 293 is the determined DNA sequence for the insertion sequence for cloning the *C. trachomatis* pmpG gene in the SKB vaccine vector.

25 SEQ ID NO: 294 is the amino acid sequence of an open reading frame of clone CT603.

SEQ ID NO: 295 is the amino acid sequence of a first open reading frame of clone CT875.

30 SEQ ID NO: 296 is the amino acid sequence of a second open reading frame of clone CT875.

SEQ ID NO: 297 is the amino acid sequence of a first open reading frame of clone CT858.

SEQ ID NO: 298 is the amino acid sequence of a second open reading frame of clone CT858.

35 SEQ ID NO: 299 is the amino acid sequence of an open reading frame of clone CT622.

- SEQ ID NO: 300 is the amino acid sequence of an open reading frame of clone CT610.
- SEQ ID NO: 301 is the amino acid sequence of an open reading frame of clone CT396.
- 5 SEQ ID NO: 302 is the amino acid sequence of an open reading frame of clone CT318.
- SEQ ID NO: 304 is the amino acid sequence for *C. trachomatis*, serovar L2 rCt529c1-125 having a modified N-terminal sequence (6-His tag).
- SEQ ID NO: 305 is the amino acid sequence for *C. trachomatis*, serovar
- 10 L2 rCt529c1-125.
- SEQ ID NO: 306 is the sense primer used in the synthesis of the PmpA(N-term) fusion protein.
- SEQ ID NO: 307 is the antisense primer used in the synthesis of the PmpA(N-term) fusion protein.
- 15 SEQ ID NO: 308 is the DNA sequence encoding the PmpA(N-term) fusion protein.
- SEQ ID NO: 309 is the amino acid sequence of the PmpA(N-term) fusion protein.
- SEQ ID NO: 310 is the sense primer used in the synthesis of the
- 20 PmpA(C-term) fusion protein.
- SEQ ID NO: 311 is the antisense primer used in the synthesis of the PmpA(C-term) fusion protein.
- SEQ ID NO: 312 is the DNA sequence encoding the PmpA(C-term) fusion protein.
- 25 SEQ ID NO: 313 is the amino acid sequence of the PmpA(C-term) fusion protein.
- SEQ ID NO: 314 is the sense primer used in the synthesis of the PmpF(N-term) fusion protein.
- SEQ ID NO: 315 is the antisense primer used in the synthesis of the
- 30 PmpF(N-term) fusion protein.
- SEQ ID NO: 316 is the DNA sequence encoding the PmpF(N-term) fusion protein.
- SEQ ID NO: 317 is the amino acid sequence of the PmpF(N-term) fusion protein.
- 35 SEQ ID NO: 318 is the sense primer used in the synthesis of the PmpF(C-term) fusion protein.

- SEQ ID NO: 319 is the antisense primer used in the synthesis of the PmpF(C-term) fusion protein.
- SEQ ID NO: 320 is the DNA sequence encoding the PmpF(C-term) fusion protein.
- 5 SEQ ID NO: 321 is the amino acid sequence of the PmpF(C-term) fusion protein.
- SEQ ID NO: 322 is the sense primer used in the synthesis of the PmpH(N-term) fusion protein.
- 10 SEQ ID NO: 323 is the antisense primer used in the synthesis of the PmpH(N-term) fusion protein.
- SEQ ID NO: 324 is the DNA sequence encoding the PmpH(N-term) fusion protein.
- SEQ ID NO: 325 is the amino acid sequence of the PmpH(N-term) fusion protein.
- 15 SEQ ID NO: 326 is the sense primer used in the synthesis of the PmpH(C-term) fusion protein.
- SEQ ID NO: 327 is the antisense primer used in the synthesis of the PmpH(C-term) fusion protein.
- 20 SEQ ID NO: 328 is the DNA sequence encoding the PmpH(C-term) fusion protein.
- SEQ ID NO: 329 is the amino acid sequence of the PmpH(C-term) fusion protein.
- SEQ ID NO: 330 is the sense primer used in the synthesis of the PmpB(1) fusion protein.
- 25 SEQ ID NO: 331 is the antisense primer used in the synthesis of the PmpB(1) fusion protein.
- SEQ ID NO: 332 is the DNA sequence encoding the PmpB(1) fusion protein.
- SEQ ID NO: 333 is the amino acid sequence of the PmpB(1) fusion protein.
- 30 SEQ ID NO: 334 is the sense primer used in the synthesis of the PmpB(2) fusion protein.
- SEQ ID NO: 335 is the antisense primer used in the synthesis of the PmpB(2) fusion protein.
- 35 SEQ ID NO: 336 is the DNA sequence encoding the PmpB(2) fusion protein.

- SEQ ID NO: 337 is the amino acid sequence of the PmpB(2) fusion protein.
- SEQ ID NO: 338 is the sense primer used in the synthesis of the PmpB(3) fusion protein.
- 5 SEQ ID NO: 339 is the antisense primer used in the synthesis of the PmpB(3) fusion protein.
- SEQ ID NO: 340 is the DNA sequence encoding the PmpB(3) fusion protein.
- 10 SEQ ID NO: 341 is the amino acid sequence of the PmpB(3) fusion protein.
- SEQ ID NO: 342 is the sense primer used in the synthesis of the PmpB(4) fusion protein.
- SEQ ID NO: 343 is the antisense primer used in the synthesis of the PmpB(4) fusion protein.
- 15 SEQ ID NO: 344 is the DNA sequence encoding the PmpB(4) fusion protein.
- SEQ ID NO: 345 is the amino acid sequence of the PmpB(4) fusion protein.
- SEQ ID NO: 346 is the sense primer used in the synthesis of the PmpC(1) fusion protein.
- 20 SEQ ID NO: 347 is the antisense primer used in the synthesis of the PmpC(1) fusion protein.
- SEQ ID NO: 348 is the DNA sequence encoding the PmpC(1) fusion protein.
- 25 SEQ ID NO: 349 is the amino acid sequence of the PmpC(1) fusion protein.
- SEQ ID NO: 350 is the sense primer used in the synthesis of the PmpC(2) fusion protein.
- SEQ ID NO: 351 is the antisense primer used in the synthesis of the PmpC(2) fusion protein.
- 30 SEQ ID NO: 352 is the DNA sequence encoding the PmpC(2) fusion protein.
- SEQ ID NO: 353 is the amino acid sequence of the PmpC(2) fusion protein.
- 35 SEQ ID NO: 354 is the sense primer used in the synthesis of the PmpC(3) fusion protein.

SEQ ID NO: 355 is the antisense primer used in the synthesis of the PmpC(3) fusion protein.

SEQ ID NO: 356 is the DNA sequence encoding the PmpC(3) fusion protein.

5 SEQ ID NO: 357 is the amino acid sequence of the PmpC(3) fusion protein.

DESCRIPTION OF THE FIGURES

Fig. 1 illustrates induction of INF- γ from a *Chlamydia*-specific T cell line activated by target cells expressing clone 4C9-18#2.

10 Fig. 2 illustrates retroviral vectors pBIB-KS1,2,3 modified to contain a Kosak translation initiation site and stop codons.

Fig. 3 shows specific lysis in a chromium release assay of P815 cells pulsed with *Chlamydia* peptides CtC7.8-12 (SEQ ID NO: 18) and CtC7.8-13 (SEQ ID NO: 19).

15 Fig. 4 shows antibody isotype titers in C57Bl/6 mice immunized with *C. trachomatis* SWIB protein.

Fig. 5 shows *Chlamydia*-specific T-cell proliferative responses in splenocytes from C3H mice immunized with *C. trachomatis* SWIB protein.

20 Fig. 6 illustrates the 5' and 3' primer sequences designed from *C. pneumoniae* which were used to isolate the SWIB and S13 genes from *C. pneumoniae*.

Figs. 7A and 7B show induction of IFN- γ from a human anti-*chlamydia* T-cell line (TCL-8) capable of cross-reacting to *C. trachomatis* and *C. pneumonia* upon activation by monocyte-derived dendritic cells expressing chlamydial proteins.

25 Fig. 8 shows the identification of T cell epitopes in Chlamydial ribosomal S13 protein with T-cell line TCL 8 EB/DC.

Fig. 9 illustrates the proliferative response of CP-21 T-cells generated against *C. pneumoniae*-infected dendritic cells to recombinant *C. pneumonia*-SWIBprotein, but not *C. trachomatis* SWIB protein.

30 Fig. 10 shows the *C. trachomatis*-specific SWIB proliferative responses of a primary T-cell line (TCT-10 EB) from an asymptomatic donor.

Fig. 11 illustrates the identification of T-cell epitope in *C. trachomatis* SWIB with an antigen specific T-cell line (TCL-10 EB).

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the diagnosis and treatment of Chlamydial infection. In one aspect, the compositions of the subject invention include polypeptides that
5 comprise at least one immunogenic portion of a *Chlamydia* antigen, or a variant thereof.

In specific embodiments, the subject invention discloses polypeptides comprising an immunogenic portion of a *Chlamydia* antigen, wherein the *Chlamydia* antigen comprises an amino acid sequence encoded by a polynucleotide molecule including a sequence selected from the group consisting of (a) nucleotide sequences
10 recited in SEQ ID NO: 1, 15, 21-25, 44-64, 66-76, 79-88, 110-119, 120, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-290 (b) the complements of said nucleotide sequences, and (c) variants of such sequences.

As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins (*i.e.*, antigens), wherein the amino acid
15 residues are linked by covalent peptide bonds. Thus, a polypeptide comprising an immunogenic portion of one of the inventive antigens may consist entirely of the immunogenic portion, or may contain additional sequences. The additional sequences may be derived from the native *Chlamydia* antigen or may be heterologous, and such sequences may (but need not) be immunogenic.

The term "polynucleotide(s)," as used herein, means a single or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases and includes DNA and corresponding RNA molecules, including HnRNA and mRNA molecules, both sense and anti-sense strands, and comprehends cDNA, genomic DNA and recombinant DNA, as well as wholly or partially synthesized polynucleotides. An HnRNA molecule
20 contains introns and corresponds to a DNA molecule in a generally one-to-one manner. An mRNA molecule corresponds to an HnRNA and DNA molecule from which the introns have been excised. A polynucleotide may consist of an entire gene, or any portion thereof. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes
25 all such operable anti-sense fragments.

An "immunogenic portion" of an antigen is a portion that is capable of reacting with sera obtained from a *Chlamydia*-infected individual (*i.e.*, generates an absorbance reading with sera from infected individuals that is at least three standard deviations above the absorbance obtained with sera from uninfected individuals, in a
30 representative ELISA assay described herein). Such immunogenic portions generally comprise at least about 5 amino acid residues, more preferably at least about 10, and

most preferably at least about 20 amino acid residues. Methods for preparing and identifying immunogenic portions of antigens of known sequence are well known in the art and include those summarized in Paul, *Fundamental Immunology*, 3rd ed., Raven Press, 1993, pp. 243-247 and references cited therein. Such techniques include

5 screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well

10 known techniques. An immunogenic portion of a native *Chlamydia* protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length polypeptide. Such screens may

15 generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound

20 antibodies detected using, for example, ¹²⁵I-labeled Protein A.

Examples of immunogenic portions of antigens contemplated by the present invention include, for example, the T cell stimulating epitopes provided in SEQ ID NO: 9, 10, 18, 19, 31, 39, 93-96, 98, 100-102, 106, 108, 138-140, 158, 167, 168, 246, 247 and 254-256. Polypeptides comprising at least an immunogenic portion of one

25 or more *Chlamydia* antigens as described herein may generally be used, alone or in combination, to detect Chlamydial infection in a patient.

The compositions and methods of the present invention also encompass variants of the above polypeptides and polynucleotide molecules. Such variants include, but are not limited to, naturally occurring allelic variants of the inventive

30 sequences. In particular, variants include other *Chlamydiae* serovars, such as serovars D, E and F, as well as the several LGV serovars which share homology to the inventive polypeptide and polynucleotide molecules described herein. Preferably, the serovar homologues show 95-99% homology to the corresponding polypeptide sequence(s) described herein.

35 A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such

that the antigenic properties of the polypeptide are retained. In a preferred embodiment, variant polypeptides differ from an identified sequence by substitution, deletion or addition of five amino acids or fewer. Such variants may generally be identified by modifying one of the above polypeptide sequences, and evaluating the antigenic properties of the modified polypeptide using, for example, the representative procedures described herein. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein. Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydrophobic nature of the polypeptide. Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydrophobic nature of the polypeptide. For example,

a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A polynucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions such that the immunogenicity of the encoded polypeptide is not diminished, relative to the native protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants as discussed below, or non-naturally occurring variants. The polypeptides provided by the present invention include variants that are encoded by polynucleotide sequences which are substantially homologous to one or more of the polynucleotide sequences specifically recited herein. "Substantial homology," as used herein, refers to polynucleotide sequences that are capable of hybridizing under moderately stringent conditions. Suitable moderately stringent conditions include prewashing in a solution of 5X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5X SSC, overnight or, in the event of cross-species homology, at 45°C with 0.5X SSC; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS. Such hybridizing polynucleotide sequences are also within the scope of this invention, as are nucleotide sequences that, due to code degeneracy, encode a polypeptide that is the same as a polypeptide of the present invention.

Two nucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acid residues in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

- Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) Fast and sensitive multiple sequence alignments on a microcomputer *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) Optimal alignments in linear space *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) The neighbor joining method. A new method for reconstructing phylogenetic trees *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) Rapid similarity searches of nucleic acid and protein data banks *Proc. Natl. Acad. Sci. USA* 80:726-730.

- Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. (U.S.A.)* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

- One illustrative example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nuc. Acids Res.* 25:3389-3402 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides and polypeptides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>) In one illustrative example, cumulative scores can be calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix can be

used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either
5 sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments, (B) of 50, expectation (E) of 10, M=5, N=-4 and a
10 comparison of both strands.

Preferably, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or amino acid sequence in the comparison window may comprise additions or deletions (i.e. gaps) of 20 percent or
15 less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the
20 total number of positions in the reference sequence (i.e. the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Therefore, the present invention provides polynucleotide and polypeptide sequences having substantial identity to the sequences disclosed herein, for example those comprising at least 50% or more sequence identity, preferably at least 55%, 60%,
25 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or higher, sequence identity compared to a polynucleotide or polypeptide sequence of this invention using the methods described herein, (e.g., BLAST analysis using standard parameters, as described below). One skilled in this art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two
30 polynucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like.

In additional embodiments, the present invention provides isolated polynucleotides or polypeptides comprising various lengths of contiguous stretches of sequence identical to or complementary to one or more of the sequences disclosed
35 herein. For example, polynucleotides and polypeptides encompassed by this invention may comprise at least about 15, 20, 30, 40, 50, 75, 100, 150, 200, 300, 400, 500 or 1000

or more contiguous nucleotides of one or more of the disclosed sequences, as well as all intermediate lengths therebetween. It will be readily understood that "intermediate lengths", in this context, means any length between the quoted values, such as 16, 17, 18, 19, *etc.*; 21, 22, 23, *etc.*; 30, 31, 32, *etc.*; 50, 51, 52, 53, *etc.*; 100, 101, 102, 103, *etc.*; 150, 151, 152, 153, *etc.*; including all integers through the 200-500; 500-1,000, and the like.

The polynucleotides of the present invention, or fragments thereof, regardless of the length of the coding sequence itself, may be combined with other DNA sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment of almost any length may be employed, with the total length preferably being limited by the ease of preparation and use in the intended recombinant DNA protocol. For example, illustrative DNA segments with total lengths of about 10,000, about 5000, about 3000, about 2,000, about 1,000, about 500, about 200, about 100, about 50 base pairs in length, and the like, (including all intermediate lengths) are contemplated to be useful in many implementations of this invention.

Also included in the scope of the present invention are alleles of the genes encoding the nucleotide sequences recited in herein. As used herein, an "allele" or "allelic sequence" is an alternative form of the gene which may result from at least one mutation in the nucleic acid sequence. Alleles may result in altered mRNAs or polypeptides whose structure or function may or may not be altered. Any given gene may have none, one, or many allelic forms. Common mutational changes which give rise to alleles are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone or in combination with the others, one or more times in a given sequence. In specific embodiments, the subject invention discloses polypeptides comprising at least an immunogenic portion of a *Chlamydia* antigen (or a variant of such an antigen), that comprises one or more of the amino acid sequences encoded by (a) a polynucleotide sequence selected from the group consisting of SEQ ID NO: 1-4, 15 21-25, 44-64, 66-76 and 79-88; (b) the complements of such DNA sequences or (c) DNA sequences substantially homologous to a sequence in (a) or (b). As discussed in the Examples below, several of the *Chlamydia* antigens disclosed herein recognize a T cell line that recognizes both *Chlamydia trachomatis* and *Chlamydia pneumoniae* infected monocyte-derived dendritic cells, indicating that they may represent an immunoreactive epitope shared by *Chlamydia trachomatis* and *Chlamydia pneumoniae*. The antigens may thus be

employed in a vaccine for both *C. trachomatis* genital tract infections and for *C. pneumonia* infections. Further characterization of these *Chlamydia* antigens from *Chlamydia trachomatis* and *Chlamydia pneumonia* to determine the extent of cross-reactivity is provided in Example 6. Additionally, Example 4 describes cDNA fragments (SEQ ID NO: 15, 16 and 33) isolated from *C. trachomatis* which encode proteins (SEQ ID NO: 17-19 and 32) capable of stimulating a *Chlamydia*-specific murine CD8+ T cell line.

In general, *Chlamydia* antigens, and polynucleotide sequences encoding such antigens, may be prepared using any of a variety of procedures. For example, polynucleotide molecules encoding *Chlamydia* antigens may be isolated from a *Chlamydia* genomic or cDNA expression library by screening with a *Chlamydia*-specific T cell line as described below, and sequenced using techniques well known to those of skill in the art. Additionally, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for *Chlamydia*-associated expression (i.e., expression that is at least two fold greater in *Chlamydia*-infected cells than in controls, as determined using a representative assay provided herein). Such screens may be performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polypeptides may be amplified from cDNA prepared from cells expressing the proteins described herein. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

Antigens may be produced recombinantly, as described below, by inserting a polynucleotide sequence that encodes the antigen into an expression vector and expressing the antigen in an appropriate host. Antigens may be evaluated for a desired property, such as the ability to react with sera obtained from a *Chlamydia*-infected individual as described herein, and may be sequenced using, for example, traditional Edman chemistry. See Edman and Berg, *Eur. J. Biochem.* 80:116-132, 1967.

Polynucleotide sequences encoding antigens may also be obtained by screening an appropriate *Chlamydia* cDNA or genomic DNA library for polynucleotide sequences that hybridize to degenerate oligonucleotides derived from partial amino acid sequences of isolated antigens. Degenerate oligonucleotide sequences for use in such a screen may be designed and synthesized, and the screen may be performed, as described (for example) in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold

Spring Harbor Laboratories, Cold Spring Harbor, NY (and references cited therein). Polymerase chain reaction (PCR) may also be employed, using the above oligonucleotides in methods well known in the art, to isolate a nucleic acid probe from a cDNA or genomic library. The library screen may then be performed using the isolated
5 probe.

An amplified portion may be used to isolate a full length gene from a suitable library (e.g., a *Chlamydia* cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is
10 size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (e.g., by nick-translation or end-labeling with ³²P) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured
15 bacterial colonies (or lawns containing phage plaques) with the labeled probe (see Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may
20 be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may
25 involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially
30 available kits may be used to perform the amplification step. Primers may be designed using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.* 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989), and software well known in the art may also be employed. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to
35 the target sequence at temperatures of about 68°C to 72°C. The amplified region may

be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the
5 known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of
10 amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res.* 19:3055-60,
15 1991). Transcription-Mediated Amplification, or TMA is another method that may be utilized for the amplification of DNA, rRNA, or mRNA, as described in Patent No. PCT/US91/03184. This autocatalytic and isothermal non-PCR based method utilizes two primers and two enzymes: RNA polymerase and reverse transcriptase. One primer contains a promoter sequence for RNA polymerase. In the first amplification, the
20 promoter-primer hybridizes to the target rRNA at a defined site. Reverse transcriptase creates a DNA copy of the target rRNA by extension from the 3' end of the promoter-primer. The RNA in the resulting complex is degraded and a second primer binds to the DNA copy. A new strand of DNA is synthesized from the end of the primer by reverse transcriptase creating double stranded DNA. RNA polymerase recognizes the promoter
25 sequence in the DNA template and initiates transcription. Each of the newly synthesized RNA amplicons re-enters the TMA process and serves as a template for a new round of replication leading to the exponential expansion of the RNA amplicon. Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

30 In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length cDNA
35 sequences may also be obtained by analysis of genomic fragments.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (see Adelman et al., *DNA* 2:183, 1983).
5 Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding a *Chlamydial* protein, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain portions may be used to prepare an encoded polypeptide, as
10 described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated *in vivo* (e.g., by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a *Chlamydial* polypeptide, and administering the transfected cells to the patient).

A portion of a sequence complementary to a coding sequence (*i.e.*, an
15 antisense polynucleotide) may also be used as a probe or to modulate gene expression. cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells of tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of a *Chlamydial* protein. Antisense technology can be used to control gene expression through triple-
20 helix formation, which compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (see Gee et al., *In Huber and Carr, Molecular and Immunologic Approaches*, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to
hybridize with a control region of a gene (e.g., promoter, enhancer or transcription
25 initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

A portion of a coding sequence, or of a complementary sequence, may also be designed as a probe or primer to detect gene expression. Probes may be labeled
30 with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and still more preferably at least 30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking
35 sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional

bases such as inosine, queosine and wybutosine, as well as acetyl- methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division, Foster City, CA, and may be operated according to the manufacturer's instructions.

As noted above, immunogenic portions of *Chlamydia* antigens may be prepared and identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3d ed., Raven Press, 1993, pp. 243-247 and references cited therein. Such techniques include screening polypeptide portions of the native antigen for immunogenic properties. The representative ELISAs described herein may generally be employed in these screens. An immunogenic portion of a polypeptide is a portion that, within such representative assays, generates a signal in such assays that is substantially similar to that generated by the full length antigen. In other words, an immunogenic portion of a *Chlamydia* antigen generates at least about 20%, and preferably about 100%, of the signal induced by the full length antigen in a model ELISA as described herein.

Portions and other variants of *Chlamydia* antigens may be generated by synthetic or recombinant means. Variants of a native antigen may generally be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis. Sections of the polynucleotide sequence may also be removed using standard techniques to permit preparation of truncated polypeptides.

Recombinant polypeptides containing portions and/or variants of a native antigen may be readily prepared from a polynucleotide sequence encoding the polypeptide using a variety of techniques well known to those of ordinary skill in the art. For example, supernatants from suitable host/vector systems which secrete
5 recombinant protein into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant protein.

10 Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides as described herein. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a polynucleotide molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher
15 eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as COS or CHO. The DNA sequences expressed in this manner may encode naturally occurring antigens, portions of naturally occurring antigens, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides
20 disclosed herein are prepared in an isolated, substantially pure, form. Preferably, the polypeptides are at least about 80% pure, more preferably at least about 90% pure and most preferably at least about 99% pure.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at
25 least one polypeptide as described herein and an unrelated sequence, such as a known *Chlamydial* protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both
30 immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein. A DNA sequence encoding a fusion protein of the present invention may be constructed using known recombinant
35 DNA techniques to assemble separate DNA sequences encoding, for example, the first and second polypeptides, into an appropriate expression vector. The 3' end of a DNA

sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8562, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. As an alternative to the use of a peptide linker sequence (when desired), one can utilize non-essential N-terminal amino acid regions (when present) on the first and second polypeptides to separate the functional domains and prevent steric hindrance.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see*, for example, Stoute et al. *New Engl. J. Med.*, 336:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises

approximately the first third of the protein (e.g., the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (see *Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In another embodiment, a *Mycobacterium tuberculosis*-derived Ra12 polynucleotide is linked to at least an immunogenic portion of a polynucleotide of this invention. Ra12 compositions and methods for their use in enhancing expression of heterologous polynucleotide sequences is described in U.S. Patent Application 60/158,585, the disclosure of which is incorporated herein by reference in its entirety. Briefly, Ra12 refers to a polynucleotide region that is a subsequence of a *Mycobacterium tuberculosis* MTB32A nucleic acid. MTB32A is a serine protease of 32 KD molecular weight encoded by a gene in virulent and avirulent strains of *M. tuberculosis*. The nucleotide sequence and amino acid sequence of MTB32A have been described (U.S. Patent Application 60/158,585; see also, Skeiky *et al.*, *Infection and Immun.* (1999) 67:3998-4007, incorporated herein by reference. In one embodiment, the Ra12 polypeptide used in the production of fusion polypeptides comprises a C-terminal fragment of the MTB32A coding sequence that is effective for enhancing the

expression and/or immunogenicity of heterologous Chlamydial antigenic polypeptides with which it is fused. In another embodiment, the Ra12 polypeptide corresponds to an approximately 14 kD C-terminal fragment of MTB32A comprising some or all of amino acid residues 192 to 323 of MTB32A.

- 5 Recombinant nucleic acids, which encode a fusion polypeptide comprising a Ra12 polypeptide and a heterologous Chlamydia polypeptide of interest, can be readily constructed by conventional genetic engineering techniques. Recombinant nucleic acids are constructed so that, preferably, a Ra12 polynucleotide sequence is located 5' to a selected heterologous Chlamydia polynucleotide sequence.
- 10 It may also be appropriate to place a Ra12 polynucleotide sequence 3' to a selected heterologous polynucleotide sequence or to insert a heterologous polynucleotide sequence into a site within a Ra12 polynucleotide sequence.

- In addition, any suitable polynucleotide that encodes a Ra12 or a portion or other variant thereof can be used in constructing recombinant fusion polynucleotides comprising Ra12 and one or more Chlamydia polynucleotides disclosed herein.
- 15 Preferred Ra12 polynucleotides generally comprise at least about 15 consecutive nucleotides, at least about 30 nucleotides, at least about 60 nucleotides, at least about 100 nucleotides, at least about 200 nucleotides, or at least about 300 nucleotides that encode a portion of a Ra12 polypeptide.

- 20 Ra12 polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a Ra12 polypeptide or a portion thereof) or may comprise a variant of such a sequence. Ra12 polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the biological activity of the encoded fusion polypeptide is not substantially diminished, relative to a fusion polypeptide comprising a native Ra12 polypeptide. Variants preferably exhibit
- 25 at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native Ra12 polypeptide or a portion thereof.

- In another aspect, the present invention provides methods for using one or more of the above polypeptides or fusion proteins (or polynucleotides encoding such polypeptides or fusion proteins) to induce protective immunity against Chlamydial infection in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease and/or infection. In other words, protective immunity may be
- 35 induced to prevent or treat Chlamydial infection.

In this aspect, the polypeptide, fusion protein or polynucleotide molecule is generally present within a pharmaceutical composition or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. Vaccines may comprise one or more of the above polypeptides and an immunostimulant, such as an adjuvant or a liposome (into which the polypeptide is incorporated). Such pharmaceutical compositions and vaccines may also contain other *Chlamydia* antigens, either incorporated into a combination polypeptide or present within a separate polypeptide.

Alternatively, a vaccine may contain polynucleotides encoding one or more polypeptides or fusion proteins as described above, such that the polypeptide is generated *in situ*. In such vaccines, the polynucleotides may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacterial and viral expression systems. Appropriate nucleic acid expression systems contain the necessary polynucleotide sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface. In a preferred embodiment, the polynucleotides may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective) virus. Techniques for incorporating polynucleotides into such expression systems are well known to those of ordinary skill in the art. The polynucleotides may also be administered as "naked" plasmid vectors as described, for example, in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (i.e., an artificial membrane vesicle). The uptake of naked

polynucleotides may be increased by incorporating the polynucleotides into and/or onto biodegradable beads, which are efficiently transported into the cells. The preparation and use of such systems is well known in the art.

In a related aspect, a polynucleotide vaccine as described above may be administered simultaneously with or sequentially to either a polypeptide of the present invention or a known *Chlamydia* antigen. For example, administration of polynucleotides encoding a polypeptide of the present invention, either "naked" or in a delivery system as described above, may be followed by administration of an antigen in order to enhance the protective immune effect of the vaccine.

Polypeptides and polynucleotides disclosed herein may also be employed in adoptive immunotherapy for the treatment of *Chlamydial* infection. Adoptive immunotherapy may be broadly classified into either active or passive immunotherapy. In active immunotherapy, treatment relies on the *in vivo* stimulation of the endogenous host immune system with the administration of immune response-modifying agents (for example, vaccines, bacterial adjuvants, and/or cytokines).

In passive immunotherapy, treatment involves the delivery of biologic reagents with established immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate anti-*Chlamydia* effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T lymphocytes (for example, CD8+ cytotoxic T-lymphocyte, CD4+ T-helper), killer cells (such as Natural Killer cells, lymphokine-activated killer cells), B cells, or antigen presenting cells (such as dendritic cells and macrophages) expressing the disclosed antigens. The polypeptides disclosed herein may also be used to generate antibodies or anti-idiotypic antibodies (as in U.S. Patent No. 4,918,164), for passive immunotherapy.

The predominant method of procuring adequate numbers of T-cells for adoptive immunotherapy is to grow immune T-cells *in vitro*. Culture conditions for expanding single antigen-specific T-cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. These *in vitro* culture conditions typically utilize intermittent stimulation with antigen, often in the presence of cytokines, such as IL-2, and non-dividing feeder cells. As noted above, the immunoreactive polypeptides described herein may be used to rapidly expand antigen-specific T cell cultures in order to generate sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast, or B-cells, may be pulsed with immunoreactive polypeptides, or polynucleotide sequence(s) may be introduced into antigen presenting cells, using a variety of standard techniques well known in the art. For example, antigen presenting

cells may be transfected or transduced with a polynucleotide sequence, wherein said sequence contains a promoter region appropriate for increasing expression, and can be expressed as part of a recombinant virus or other expression system. Several viral vectors may be used to transduce an antigen presenting cell, including pox virus, vaccinia virus, and adenovirus; also, antigen presenting cells may be transfected with polynucleotide sequences disclosed herein by a variety of means, including gene-gun technology, lipid-mediated delivery, electroporation, osmotic shock, and particulate delivery mechanisms, resulting in efficient and acceptable expression levels as determined by one of ordinary skill in the art. For cultured T-cells to be effective in therapy, the cultured T-cells must be able to grow and distribute widely and to survive long term *in vivo*. Studies have demonstrated that cultured T-cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (see, for example, Cheever, M., *et al*, "Therapy With Cultured T Cells: Principles Revisited," *Immunological Reviews*, 157:177, 1997).

The polypeptides disclosed herein may also be employed to generate and/or isolate chlamydial-reactive T-cells, which can then be administered to the patient. In one technique, antigen-specific T-cell lines may be generated by *in vivo* immunization with short peptides corresponding to immunogenic portions of the disclosed polypeptides. The resulting antigen specific CD8+ or CD4+ T-cell clones may be isolated from the patient, expanded using standard tissue culture techniques, and returned to the patient.

Alternatively, peptides corresponding to immunogenic portions of the polypeptides may be employed to generate *Chlamydia* reactive T cell subsets by selective *in vitro* stimulation and expansion of autologous T cells to provide antigen-specific T cells which may be subsequently transferred to the patient as described, for example, by Chang *et al*, (*Crit. Rev. Oncol. Hematol.*, 22(3), 213, 1996). Cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as Isolex™ System, available from Nexell Therapeutics, Inc. Irvine, CA. The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

In other embodiments, T-cell and/or antibody receptors specific for the polypeptides disclosed herein can be cloned, expanded, and transferred into other vectors or effector cells for use in adoptive immunotherapy. In particular, T cells may

be transfected with the appropriate genes to express the variable domains from chlamydia specific monoclonal antibodies as the extracellular recognition elements and joined to the T cell receptor signaling chains, resulting in T cell activation, specific lysis, and cytokine release. This enables the T cell to redirect its specificity in an MHC-independent manner. See for example, Eshhar, Z., *Cancer Immunol Immunother*, 45(3-4):131-6, 1997 and Hwu, P., et al, *Cancer Res*, 55(15):3369-73, 1995. Another embodiment may include the transfection of chlamydia antigen specific alpha and beta T cell receptor chains into alternate T cells, as in Cole, DJ, et al, *Cancer Res*, 55(4):748-52, 1995.

In a further embodiment, syngeneic or autologous dendritic cells may be pulsed with peptides corresponding to at least an immunogenic portion of a polypeptide disclosed herein. The resulting antigen-specific dendritic cells may either be transferred into a patient, or employed to stimulate T cells to provide antigen-specific T cells which may, in turn, be administered to a patient. The use of peptide-pulsed dendritic cells to generate antigen-specific T cells and the subsequent use of such antigen-specific T cells to eradicate disease in a murine model has been demonstrated by Cheever et al, *Immunological Reviews*, 157:177, 1997). Additionally, vectors expressing the disclosed polynucleotides may be introduced into stem cells taken from the patient and clonally propagated *in vitro* for autologous transplant back into the same patient.

Within certain aspects, polypeptides, polynucleotides, T cells and/or binding agents disclosed herein may be incorporated into pharmaceutical compositions or immunogenic compositions (*i.e.*, vaccines). Alternatively, a pharmaceutical composition may comprise an antigen-presenting cell (*e.g.* a dendritic cell) transfected with a *Chlamydial* polynucleotide such that the antigen presenting cell expresses a *Chlamydial* polypeptide. Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and an immunostimulant. An immunostimulant may be any substance that enhances or potentiates an immune response to an exogenous antigen. Examples of immunostimulants include adjuvants, biodegradable microspheres (*e.g.*, polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic

portions of other *Chlamydial* antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope.

In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, adenovirus, baculovirus, togavirus, bacteriophage, and the like), which often involves the use of a non-pathogenic (defective), replication competent virus.

For example, many viral expression vectors are derived from viruses of the retroviridae family. This family includes the murine leukemia viruses, the mouse mammary tumor viruses, the human foamy viruses, Rous sarcoma virus, and the immunodeficiency viruses, including human, simian, and feline. Considerations when designing retroviral expression vectors are discussed in Comstock *et al.* (1997).

Excellent murine leukemia virus (MLV)-based viral expression vectors have been developed by Kim *et al.* (1998). In creating the MLV vectors, Kim *et al.* found that the entire *gag* sequence, together with the immediate upstream region, could be deleted without significantly affecting viral packaging or gene expression. Further, it was found that nearly the entire U3 region could be replaced with the immediately-early promoter of human cytomegalovirus without deleterious effects. Additionally, MCR and internal ribosome entry sites (IRES) could be added without adverse effects. Based on their observations, Kim *et al.* have designed a series of MLV-based expression vectors comprising one or more of the features described above.

As more has been learned about human foamy virus (HFV), characteristics of HFV that are favorable for its use as an expression vector have been discovered. These characteristics include the expression of pol by splicing and start of

translation at a defined initiation codon. Other aspects of HFV viral expression vectors are reviewed in Bodem *et al.* (1997).

Murakami *et al.* (1997) describe a Rous sarcoma virus (RSV)-based replication-competent avian retrovirus vectors, IR1 and IR2 to express a heterologous gene at a high level. In these vectors, the IRES derived from encephalomyocarditis virus (EMCV) was inserted between the *env* gene and the heterologous gene. The IR1 vector retains the splice-acceptor site that is present downstream of the *env* gene while the IR2 vector lacks it. Murakami *et al.* have shown high level expression of several different heterologous genes by these vectors.

Recently, a number of lentivirus-based retroviral expression vectors have been developed. Kafri *et al.* (1997) have shown sustained expression of genes delivered directly into liver and muscle by a human immunodeficiency virus (HIV)-based expression vector. One benefit of the system is the inherent ability of HIV to transduce non-dividing cells. Because the viruses of Kafri *et al.* are pseudotyped with vesicular stomatitis virus G glycoprotein (VSVG), they can transduce a broad range of tissues and cell types.

A large number of adenovirus-based expression vectors have been developed, primarily due to the advantages offered by these vectors in gene therapy applications. Adenovirus expression vectors and methods of using such vectors are the subject of a number of United States patents, including United States Patent No. 5,698,202, United States Patent No. 5,616,326, United States Patent No. 5,585,362, and United States Patent No. 5,518,913, all incorporated herein by reference.

Additional adenoviral constructs are described in Khatri *et al.* (1997) and Tomanin *et al.* (1997). Khatri *et al.* describe novel ovine adenovirus expression vectors and their ability to infect bovine nasal turbinate and rabbit kidney cells as well as a range of human cell type, including lung and foreskin fibroblasts as well as liver, prostate, breast, colon and retinal lines. Tomanin *et al.* describe adenoviral expression vectors containing the T7 RNA polymerase gene. When introduced into cells containing a heterologous gene operably linked to a T7 promoter, the vectors were able to drive gene expression from the T7 promoter. The authors suggest that this system may be useful for the cloning and expression of genes encoding cytotoxic proteins.

Poxviruses are widely used for the expression of heterologous genes in mammalian cells. Over the years, the vectors have been improved to allow high expression of the heterologous gene and simplify the integration of multiple heterologous genes into a single molecule. In an effort to diminish cytopathic effects and to increase safety, vaccinia virus mutant and other poxviruses that undergo abortive

infection in mammalian cells are receiving special attention (Oertli *et al.*, 1997). The use of poxviruses as expression vectors is reviewed in Carroll and Moss (1997).

Togaviral expression vectors, which includes alphaviral expression vectors have been used to study the structure and function of proteins and for protein production purposes. Attractive features of togaviral expression vectors are rapid and efficient gene expression, wide host range, and RNA genomes (Huang, 1996). Also, recombinant vaccines based on alphaviral expression vectors have been shown to induce a strong humoral and cellular immune response with good immunological memory and protective effects (Tubulekas *et al.*, 1997). Alphaviral expression vectors and their use are discussed, for example, in Lundstrom (1997).

In one study, Li and Garoff (1996) used Semliki Forest virus (SFV) expression vectors to express retroviral genes and to produce retroviral particles in BHK-21 cells. The particles produced by this method had protease and reverse transcriptase activity and were infectious. Furthermore, no helper virus could be detected in the virus stocks. Therefore, this system has features that are attractive for its use in gene therapy protocols.

Baculoviral expression vectors have traditionally been used to express heterologous proteins in insect cells. Examples of proteins include mammalian chemokine receptors (Wang *et al.*, 1997), reporter proteins such as green fluorescent protein (Wu *et al.*, 1997), and FLAG fusion proteins (Wu *et al.*, 1997; Koh *et al.*, 1997). Recent advances in baculoviral expression vector technology, including their use in virion display vectors and expression in mammalian cells is reviewed by Possee (1997). Other reviews on baculoviral expression vectors include Jones and Morikawa (1996) and O'Reilly (1997).

Other suitable viral expression systems are disclosed, for example, in Fisher-Hoch *et al.*, *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner *et al.*, *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner *et al.*, *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld *et al.*, *Science* 252:431-434, 1991; Kolls *et al.*, *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler *et al.*, *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman *et al.*, *Circulation* 88:2838-2848, 1993; and Guzman *et al.*, *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. In other systems, the DNA may be introduced as "naked" DNA, as described, for example, in Ulmer *et al.*, *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The

uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

It will be apparent that a vaccine may comprise a polynucleotide and/or a polypeptide component, as desired. It will also be apparent that a vaccine may contain pharmaceutically acceptable salts of the polynucleotides and/or polypeptides provided herein. Such salts may be prepared from pharmaceutically acceptable non-toxic bases, including organic bases (*e.g.*, salts of primary, secondary and tertiary amines and basic amino acids) and inorganic bases (*e.g.*, sodium, potassium, lithium, ammonium, calcium and magnesium salts). While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.*, polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (*e.g.*, neutral buffered saline or phosphate buffered saline), carbohydrates (*e.g.*, glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, bacteriostats, chelating agents such as EDTA or glutathione, adjuvants (*e.g.*, aluminum hydroxide), solutes that render the formulation isotonic, hypotonic or weakly hypertonic with the blood of a recipient, suspending agents, thickening agents and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of immunostimulants may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant

and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, under select circumstances, the adjuvant composition may be designed to induce an immune response predominantly of the Th1 type or Th2 type. High levels of Th1-type cytokines (*e.g.*, IFN- γ , TNF α , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (*e.g.*, IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Corixa Corporation (Seattle, WA; *see* US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555 and WO 99/33488. Immunostimulatory DNA sequences are also described, for example, by Sato et al., *Science* 273:352, 1996. Another preferred adjuvant is a saponin, preferably QS21 (Aquila Biopharmaceuticals Inc., Framingham, MA), which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprise an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210.

Other preferred adjuvants include Montanide ISA 720 (Seppic, France), SAF (Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series of adjuvants (e.g., SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart, Belgium), Detox (Corixa Corporation; Seattle, WA), RC-529 (Corixa Corporation; Seattle, WA) and other aminoalkyl glucosaminide 4-phosphates (AGPs), such as those described in pending U.S. Patent Application Serial Nos. 08/853,826 and 09/074,720, the disclosures of which are incorporated herein by reference in their entireties.

Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immunostimulant and a suitable carrier or excipient. The compositions described herein may be administered as part of a sustained release formulation (i.e., a formulation such as a capsule, sponge or gel (composed of polysaccharides, for example) that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology (see, e.g., Coombes et al., *Vaccine* 14:1429-1438, 1996) and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane.

Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. Such carriers include microparticles of poly(lactide-co-glycolide), as well as polyacrylate, latex, starch, cellulose and dextran. Other delayed-release carriers include supramolecular biovectors, which comprise a non-liquid hydrophilic core (e.g., a cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (see e.g., U.S. Patent No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific immune response that targets *Chlamydia*-infected cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the

antigen, to improve activation and/or maintenance of the T cell response, to have anti-*Chlamydia* effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, and may be autologous, allogeneic, syngeneic or
5 xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic
10 immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency, and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-
15 surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see* Zitvogel et al., *Nature Med.* 4:594-600, 1998).

20 Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells
25 harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature"
30 cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor and mannose receptor. The mature
35 phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and

class II MHC, adhesion molecules (e.g., CD54 and CD11) and costimulatory molecules (e.g., CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide encoding a *Chlamydial* protein (or portion or other variant thereof) such that the *Chlamydial* polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the *Chlamydial* polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (e.g., vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (e.g., a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

Routes and frequency of administration of pharmaceutical compositions and vaccines, as well as dosage, will vary from individual to individual. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 3 doses may be administered for a 1-36 week period. Preferably, 3 doses are administered, at intervals of 3-4 months, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that, when administered as described above, is capable of raising an immune response in an immunized patient sufficient to protect the patient from *Chlamydial* infection for at least 1-2 years. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 µg. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic galactide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a *Chlamydial* protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

In another aspect, the present invention provides methods for using the polypeptides described above to diagnose Chlamydial infection. In this aspect, methods are provided for detecting Chlamydial infection in a biological sample, using one or more of the above polypeptides, either alone or in combination. For clarity, the term "polypeptide" will be used when describing specific embodiments of the inventive diagnostic methods. However, it will be clear to one of skill in the art that the fusion proteins of the present invention may also be employed in such methods.

As used herein, a "biological sample" is any antibody-containing sample obtained from a patient. Preferably, the sample is whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid or urine. More preferably, the sample is a blood, serum or plasma sample obtained from a patient. The polypeptides are used in an assay, as described below, to determine the presence or absence of antibodies to the polypeptide(s) in the sample, relative to a predetermined cut-off value. The presence of such antibodies indicates previous sensitization to *Chlamydia* antigens which may be indicative of *Chlamydia*-infection.

In embodiments in which more than one polypeptide is employed, the polypeptides used are preferably complementary (i.e., one component polypeptide will tend to detect infection in samples where the infection would not be detected by another

component polypeptide). Complementary polypeptides may generally be identified by using each polypeptide individually to evaluate serum samples obtained from a series of patients known to be infected with *Chlamydia*. After determining which samples test positive (as described below) with each polypeptide, combinations of two or more polypeptides may be formulated that are capable of detecting infection in most, or all, of the samples tested.

A variety of assay formats are known to those of ordinary skill in the art for using one or more polypeptides to detect antibodies in a sample. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988, which is incorporated herein by reference. In a preferred embodiment, the assay involves the use of polypeptide immobilized on a solid support to bind to and remove the antibody from the sample. The bound antibody may then be detected using a detection reagent that contains a reporter group. Suitable detection reagents include antibodies that bind to the antibody/polypeptide complex and free polypeptide labeled with a reporter group (e.g., in a semi-competitive assay). Alternatively, a competitive assay may be utilized, in which an antibody that binds to the polypeptide is labeled with a reporter group and allowed to bind to the immobilized antigen after incubation of the antigen with the sample. The extent to which components of the sample inhibit the binding of the labeled antibody to the polypeptide is indicative of the reactivity of the sample with the immobilized polypeptide.

The solid support may be any solid material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate, or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681.

The polypeptides may be bound to the solid support using a variety of techniques known to those of ordinary skill in the art. In the context of the present invention, the term "bound" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Binding by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the polypeptide, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and 1 day. In general,

contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of polypeptide ranging from about 10 ng to about 1 µg, and preferably about 100 ng, is sufficient to bind an adequate amount of antigen.

Covalent attachment of polypeptide to a solid support may generally be
5 achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the polypeptide. For example, the polypeptide may be bound to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the polypeptide (*see*,
10 *e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is an enzyme linked immunosorbent assay (ELISA). This assay may be performed by first contacting a polypeptide antigen that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that antibodies to the polypeptide within the sample are allowed
15 to bind to the immobilized polypeptide. Unbound sample is then removed from the immobilized polypeptide and a detection reagent capable of binding to the immobilized antibody-polypeptide complex is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific detection reagent.

More specifically, once the polypeptide is immobilized on the support as
20 described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin (BSA) or Tween 20™ (Sigma Chemical Co., St. Louis, MO) may be employed. The immobilized polypeptide is then incubated with the sample, and
25 antibody is allowed to bind to the antigen. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of antibody within an HGE-infected sample. Preferably, the contact time is sufficient to achieve a level of binding that is at least 95% of that achieved at
30 equilibrium between bound and unbound antibody. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support
35 with an appropriate buffer, such as PBS containing 0.1% Tween 20™. Detection reagent may then be added to the solid support. An appropriate detection reagent is any

compound that binds to the immobilized antibody-polypeptide complex and that can be detected by any of a variety of means known to those in the art. Preferably, the detection reagent contains a binding agent (such as, for example, Protein A, Protein G, immunoglobulin, lectin or free antigen) conjugated to a reporter group. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of binding agent to reporter group may be achieved using standard methods known to those of ordinary skill in the art. Common binding agents may also be purchased conjugated to a variety of reporter groups from many commercial sources (e.g., Zymed Laboratories, San Francisco, CA, and Pierce, Rockford, IL).

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound antibody. An appropriate amount of time may generally be determined from the manufacturer's instructions or by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of anti-*Chlamydia* antibodies in the sample, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antigen is incubated with samples from an uninfected patient. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for *Chlamydia*-infection. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, pp. 106-107. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (i.e., sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off

value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for Chlamydial infection.

In a related embodiment, the assay is performed in a rapid flow-through or strip test format, wherein the antigen is immobilized on a membrane, such as nitrocellulose. In the flow-through test, antibodies within the sample bind to the immobilized polypeptide as the sample passes through the membrane. A detection reagent (*e.g.*, protein A-colloidal gold) then binds to the antibody-polypeptide complex as the solution containing the detection reagent flows through the membrane. The detection of bound detection reagent may then be performed as described above. In the strip test format, one end of the membrane to which polypeptide is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing detection reagent and to the area of immobilized polypeptide. Concentration of detection reagent at the polypeptide indicates the presence of anti-*Chlamydia* antibodies in the sample. Typically, the concentration of detection reagent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of polypeptide immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of antibodies that would be sufficient to generate a positive signal in an ELISA, as discussed above. Preferably, the amount of polypeptide immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount (*e.g.*, one drop) of patient serum or blood.

Of course, numerous other assay protocols exist that are suitable for use with the polypeptides of the present invention. The above descriptions are intended to be exemplary only. One example of an alternative assay protocol which may be usefully employed in such methods is a Western blot, wherein the proteins present in a biological sample are separated on a gel, prior to exposure to a binding agent. Such techniques are well known to those of skill in the art.

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a *Chlamydial* protein. As used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically

bind" to a *Chlamydial* protein if it reacts at a detectable level (within, for example, an ELISA) with a *Chlamydial* protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a *Chlamydial* infection using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a *Chlamydial* protein will generate a signal indicating the presence of a *Chlamydial* infection in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without infection. To determine whether a binding agent satisfies this requirement, biological samples (e.g., blood, sera, sputum urine and/or tissue biopsies) from patients with and without *Chlamydial* infection (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen

without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane,

Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or
5 more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{125}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria
10 toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a
15 substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an
20 antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents,
25 which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups,
30 sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of
35 different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction

of a disulfide bond (e.g., U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (e.g., U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (e.g., U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (e.g., U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (e.g., U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (e.g., U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (e.g., U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (e.g., U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in site-specific regions by appropriate methods. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density, and the rate of clearance of the antibody.

Antibodies may be used in diagnostic tests to detect the presence of *Chlamydia* antigens using assays similar to those detailed above and other techniques well known to those of skill in the art, thereby providing a method for detecting Chlamydial infection in a patient.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions

thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify *Chlamydia*-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a polypeptide of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a polypeptide of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule encoding one of the polypeptides disclosed herein. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule encoding one of the polypeptides disclosed herein. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis *et al. Ibid*; Ehrlich, *Ibid*). Primers or probes may thus be used to detect *Chlamydia*-specific sequences in biological samples. DNA probes or primers comprising oligonucleotide sequences described above may be used alone or in combination with each other.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLE I

ISOLATION OF DNA SEQUENCES ENCODING *CHLAMYDIA* ANTIGENS

Chlamydia antigens of the present invention were isolated by expression cloning of a genomic DNA library of *Chlamydia trachomatis* LGV II essentially as described by Sanderson et al. (*J. Exp. Med.*, 1995, 182:1751-1757) and were shown to induce PBMC proliferation and IFN- γ in an immunoreactive T cell line.

A *Chlamydia*-specific T cell line was generated by stimulating PBMCs from a normal donor with no history of chlamydial genital tract infection with elementary bodies of *Chlamydia trachomatis* LGV II. This T cell line, referred to as TCL-8, was found to recognize both *Chlamydia trachomatis* and *Chlamydia pneumonia* infected monocyte-derived dendritic cells.

A randomly sheared genomic library of *Chlamydia trachomatis* LGV II was constructed in Lambda ZAP (Stratagene, La Jolla, CA) and the amplified library plated out in 96 well microtiter plates at a density of 30 clones/well. Bacteria were induced to express recombinant protein in the presence of 2 mM IPTG for 3 h, then pelleted and resuspended in 200 μ l of RPMI 10% FBS. 10 μ l of the induced bacterial suspension was transferred to 96 well plates containing autologous monocyte-derived dendritic cells. After a 2 h incubation, dendritic cells were washed to remove free *E. coli* and *Chlamydia*-specific T cells were added. Positive *E. coli* pools were identified by determining IFN- γ production and proliferation of the T cells in response to the pools.

Four positive pools were identified, which were broken down to yield four pure clones (referred to as 1-B1-66, 4-D7-28, 3-G3-10 and 10-C10-31), with insert sizes of 481 bp, 183 bp, 110 bp and 1400 bp, respectively. The determined DNA sequences for 1-B1-66, 4-D7-28, 3-G3-10 and 10-C10-31 are provided in SEQ ID NO: 1-4, respectively. Clone 1-B1-66 is approximately in region 536690 of the *C. trachomatis* genome (NCBI *C. trachomatis* database). Within clone 1-B1-66, an open reading frame (ORF) has been identified (nucleotides 115 - 375) that encodes a previously identified 9 kDa protein (Stephens, et al. Genbank Accession No. AE001320), the sequence of which is provided in SEQ ID NO: 5). Clone 4-D7-28 is a smaller region of the same ORF (amino acids 22-82 of 1-B1-66). Clone 3-G3-10 is approximately in region 74559 of the *C. trachomatis* genome. The insert is cloned in the antisense orientation with respect to its orientation in the genome. The clone 10-C10-31 contains an open reading frame that corresponds to a previously published sequence for S13 ribosomal protein from *Chlamydia trachomatis* (Gu, L. et al. *J. Bacteriology*, 177:2594-2601, 1995). The predicted protein sequences for 4-D7-28 and

10-C10-31 are provided in SEQ ID NO: 6 and 12, respectively. Predicted protein sequences for 3-G3-10 are provided in SEQ ID NO: 7-11.

In a related series of screening studies, an additional T cell line was used to screen the genomic DNA library of *Chlamydia trachomatis* LGV II described above.

- 5 A *Chlamydia*-specific T cell line (TCT-1) was derived from a patient with a chlamydial genital tract infection by stimulating patient PBMC with autologous monocyte-derived dendritic cells infected with elementary bodies of *Chlamydia trachomatis* LGV II. One clone, 4C9-18 (SEQ ID NO: 21), containing a 1256 bp insert, elicited a specific immune response, as measured by standard proliferation assays, from the *Chlamydia*-
10 specific T cell line TCT-1. Subsequent analysis revealed this clone to contain three known sequences: lipoamide dehydrogenase (Genbank Accession No. AE001326), disclosed in SEQ ID NO: 22; a hypothetical protein CT429 (Genbank Accession No. AE001316), disclosed in SEQ ID NO: 23; and part of an open reading frame of ubiquinone methyltransferase CT428 (Genbank Accession No. AE001316), disclosed in
15 SEQ ID NO: 24.

In further studies involving clone 4C9-18 (SEQ ID NO: 21), the full-length amino acid sequence for lipoamide dehydrogenase (SEQ ID NO: 22) from *C. trachomatis* (LGV II) was expressed in clone Ctl2-LPDA-FL, as disclosed in SEQ ID NO: 90.

- 20 To further characterize the open reading frame containing the T cell stimulating epitope(s), a cDNA fragment containing nucleotides 1-695 of clone 4C9-18 with a cDNA sequence encoding a 6X-Histidine tag on the amino terminus was subcloned into the NdeI/EcoRI site of the pET17b vector (Novagen, Madison, WI), referred to as clone 4C9-18#2 BL21 pLysS (SEQ ID NO: 25, with the corresponding
25 amino acid sequence provided in SEQ ID NO: 26) and transformed into *E. coli*. Selective induction of the transformed *E. coli* with 2 mM IPTG for three hours resulted in the expression of a 26 kDa protein from clone 4C9-18#2 BL21 pLysS, as evidenced by standard Coomassie-stained SDS-PAGE. To determine the immunogenicity of the protein encoded by clone 4C9-18#2 BL21 pLysS, *E. coli* expressing the 26 kDa protein
30 were titrated onto 1×10^4 monocyte-derived dendritic cells and incubated for two hours. The dendritic cell cultures were washed and 2.5×10^4 T cells (TCT-1) added and allowed to incubate for an additional 72 hours, at which time the level of IFN- γ in the culture supernatant was determined by ELISA. As shown in Fig. 1, the T-cell line TCT-1 was found to respond to induced cultures as measured by IFN-g, indicating a
35 *Chlamydia*-specific T-cell response against the lipoamide dehydrogenase sequence.

Similarly, the protein encoded by clone 4C9-18#2 BL21 pLysS was shown to stimulate the TCT-1 T-cell line by standard proliferation assays.

Subsequent studies to identify additional *Chlamydia trachomatis* antigens using the above-described CD4+ T-cell expression cloning technique yielded additional clones. The TCT-1 and TCL-8 *Chlamydia*-specific T-cell lines, as well as the TCP-21 T-cell line were utilized to screen the *Chlamydia trachomatis* LGVII genomic library. The TCP-21 T-cell line was derived from a patient having a humoral immune response to *Chlamydia pneumoniae*. The TCT-1 cell line identified 37 positive pools, the TCT-3 cell line identified 41 positive pools and the TCP-21 cell line identified 2 positive pools. The following clones were derived from 10 of these positive pools. Clone 11-A3-93 (SEQ ID NO: 64), identified by the TCP-21 cell line, is a 1339 bp genomic fragment sharing homology to the HAD superfamily (CT103). The second insert in the same clone shares homology with the fab I gene (CT104) present on the complementary strand. Clone 11-C12-91 (SEQ ID NO: 63), identified using the TCP-21 cell line, has a 269 bp insert that is part of the OMP2 gene (CT443) and shares homology with the 60 kDa cysteine rich outer membrane protein of *C. pneumoniae*.

Clone 11-G10-46, (SEQ ID NO: 62), identified using the TCT-3 cell line, contains a 688 bp insert that shares homology to the hypothetical protein CT610. Clone 11-G1-34, (SEQ ID NO: 61), identified using the TCT-3 cell line, has two partial open reading frames (ORF) with an insert size of 1215 bp. One ORF shares homology to the malate dehydrogenase gene (CT376), and the other ORF shares homology to the glycogen hydrolase gene (CT042). Clone 11-H3-68, (SEQ ID NO: 60), identified using the TCT-3 cell line, has two ORFs with a total insert size of 1180 bp. One partial ORF encodes the plasmid-encoded PGP6-D virulence protein while the second ORF is a complete ORF for the L1 ribosomal gene (CT318). Clone 11-H4-28, (SEQ ID NO: 59), identified using the TCT-3 cell line, has an insert size of 552 bp and is part of the ORF for the dnaK gene (CT396). Clone 12-B3-95, (SEQ ID NO: 58), identified using the TCT-1 cell line, has an insert size of 463 bp and is a part of the ORF for the lipoamide dehydrogenase gene (CT557). Clones 15-G1-89 and 12-B3-95 are identical, (SEQ ID NO: 55 and 58, respectively), identified using the TCT-1 cell line, has an insert size of 463 bp and is part of the ORF for the lipoamide dehydrogenase gene (CT557). Clone 12-G3-83, (SEQ ID NO: 57), identified using the TCT-1 cell line, has an insert size of 1537 bp and has part of the ORF for the hypothetical protein CT622.

Clone 23-G7-68, (SEQ ID NO: 79), identified using the TCT-3 cell line, contains a 950 bp insert and contains a small part of the L11 ribosomal ORF, the entire ORF for L1 ribosomal protein and a part of the ORF for L10 ribosomal protein. Clone

22-F8-91, (SEQ ID NO: 80), identified using the TCT-1 cell line, contains a 395 bp insert that contains a part of the pmpC ORF on the complementary strand of the clone. Clone 21-E8-95, (SEQ ID NO: 81), identified using the TCT-3 cell line, contains a 2,085 bp insert which contains part of CT613 ORF, the complete ORF for CT612, the complete ORF for CT611 and part of the ORF for CT610. Clone 19-F12-57, (SEQ ID NO: 82), identified using the TCT-3 cell line, contains a 405 bp insert which contains part of the CT 858 ORF and a small part of the recA ORF. Clone 19-F12-53, (SEQ ID NO: 83), identified using the TCT-3 cell line, contains a 379 bp insert that is part of the ORF for CT455 encoding glutamyl tRNA synthetase. Clone 19-A5-54, (SEQ ID NO: 84), identified using the TCT-3 cell line, contains a 715 bp insert that is part of the ORF3 (complementary strand of the clone) of the cryptic plasmid. Clone 17-E11-72, (SEQ ID NO: 85), identified using the TCT-1 cell line, contains a 476 bp insert that is part of the ORF for Opp₂ and pmpD. The pmpD region of this clone is covered by the pmpD region of clone 15-H2-76. Clone 17-C1-77, (SEQ ID NO: 86), identified using the TCT-3 cell line, contains a 1551 bp insert that is part of the CT857 ORF, as well as part of the CT858 ORF. Clone 15-H2-76, (SEQ ID NO: 87), identified using the TCT-1 cell line, contains a 3,031 bp insert that contains a large part of the pmpD ORF, part of the CT089 ORF, as well as part of the ORF for SycE. Clone 15-A3-26, (SEQ ID NO: 88), contains a 976 bp insert that contains part of the ORF for CT858. Clone 17-G4-36, (SEQ ID NO: 267), identified using the TCT-10 cell line, contains a 680 bp insert that is in frame with beta-gal in the plasmid and shares homology to part of the ORF for DNA-directed RNA polymerase beta subunit (CT315 in SerD).

Several of the clones described above share homology to various polymorphic membrane proteins. The genomic sequence of *Chlamydia trachomatis* contains a family of nine polymorphic membrane protein genes, referred to as pmp. These genes are designated pmpA, pmpB, pmpC, pmpD, pmpE, pmpF, pmpG, pmpH and pmpI. Proteins expressed from these genes are believed to be of biological relevance in generating a protective immune response to a *Chlamydial* infection. In particular, pmpC, pmpD, pmpE and pmpI contain predictable signal peptides, suggesting they are outer membrane proteins, and therefore, potential immunological targets.

Based on the *Chlamydia trachomatis* LGVII serovar sequence, primer pairs were designed to PCR amplify the full-length fragments of pmpC, pmpD, pmpE, pmpG, pmpH and pmpI. The resulting fragments were subcloned into the DNA vaccine vector JA4304 or JAL, which is JA4304 with a modified linker (SmithKline Beecham, London, England). Specifically, PmpC was subcloned into the JAL vector using the 5'

oligo GAT AGG CGC GCC GCA ATC ATG AAA TTT ATG TCA GCT ACT GCT G and the 3' oligo CAG AAC GCG TTT AGA ATG TCA TAC GAG CAC CGC A, as provided in SEQ ID NO: 197 and 198, respectively. PCR amplification of the gene under conditions well known in the art and ligation into the 5' ASCI/3' MluI sites of the

5 JAL vector was completed after inserting the short nucleotide sequence GCAATC (SEQ ID NO: 199) upstream of the ATG to create a Kozak-like sequence. The resulting expression vector contained the full-length pmpC gene comprising 5325 nucleotides (SEQ ID NO: 173) containing the hypothetical signal sequence, which encodes a 187 kD protein (SEQ ID NO: 179). The pmpD gene was subcloned into the JA4304 vaccine

10 vector following PCR amplification of the gene using the following oligos: 5' oligo- TGC AAT CAT GAG TTC GCA GAA AGA TAT AAA AAG C (SEQ ID NO: 200) and 3' oligo- CAG AGC TAG CTT AAA AGA TCA ATC GCA ATC CAG TAT TC (SEQ ID NO: 201). The gene was ligated into the a 5' blunted HIII/3' MluI site of the JA4304 vaccine vector using standard techniques well known in the art. The CAATC

15 (SEQ ID NO: 202) was inserted upstream of the ATG to create a Kozak-like sequence. This clone is unique in that the last threonine of the HindIII site is missing due to the blunting procedure, as is the last glycine of the Kozak-like sequence. The insert, a 4593 nucleotide fragment (SEQ ID NO: 172) is the full-length gene for pmpD containing the hypothetical signal sequence, which encodes a 161 kD protein (SEQ ID NO: 178).

20 PmpE was subcloned into the JA4304 vector using the 5' oligo- TGC AAT CAT GAA AAA AGC GTT TTT CTT TTT C (SEQ ID NO: 203), and the 3' oligo- CAG AAC GCG TCT AGA ATC GCA GAG CAA TTT C (SEQ ID NO: 204). Following PCR amplification, the gene was ligated into the 5' blunted HIII/3' MluI site of JA4304. To facilitate this, a short nucleotide sequence, TGCAATC (SEQ ID NO: 293), was added

25 upstream of the initiation codon for creating a Kozak-like sequence and reconstituting the HindIII site. The insert is the full-length pmpE gene (SEQ ID NO: 171) containing the hypothetical signal sequence. The pmpE gene encodes a 105 kD protein (SEQ ID NO: 177). The pmpG gene was PCR amplified using the 5' oligo- GTG CAA TCA TGA TTC CTC AAG GAA TTT ACG (SEQ ID NO: 205), and the 3' oligo- CAG

30 AAC GCG TTT AGA ACC GGA CTT TAC TTC C (SEQ ID NO: 206) and subcloned into the JA4304 vector. Similar cloning strategies were followed for the pmpI and pmpK genes. In addition, primer pairs were designed to PCR amplify the full-length or overlapping fragments of the pmp genes, which were then subcloned for protein expression in the pET17b vector (Novagen, Madison, WI) and transfected into E. coli

35 BL21 pLysS for expression and subsequent purification utilizing the histidine-nickel chromatographic methodology provided by Novagen. Several of the genes encoding

the recombinant proteins, as described below, lack the native signal sequence to facilitate expression of the protein. Full-length protein expression of pmpC was accomplished through expression of two overlapping fragments, representing the amino and carboxy termini. Subcloning of the pmpC-amino terminal portion, which lacks the signal sequence, (SEQ ID NO: 187, with the corresponding amino acid sequence provided in SEQ ID NO: 195) used the 5' oligo- CAG ACA TAT GCA TCA CCA TCA CCA TCA CGA GGC GAG CTC GAT CCA AGA TC (SEQ ID NO: 207), and the 3' oligo- CAG AGG TAC CTC AGA TAG CAC TCT CTC CTA TTA AAG TAG G (SEQ ID NO: 208) into the 5' NdeI/3' KPN cloning site of the vector. The carboxy terminus portion of the gene, pmpC-carboxy terminal fragment (SEQ ID NO: 186, with the corresponding amino acid sequence provided in SEQ ID NO: 194), was subcloned into the 5' NheI/3' KPN cloning site of the expression vector using the following primers: 5' oligo- CAG AGC TAG CAT GCA TCA CCA TCA CCA TCA CGT TAA GAT TGA GAA CTT CTC TGG C (SEQ ID NO: 209), and 3' oligo- CAG AGG TAC CTT AGA ATG TCA TAC GAG CAC CGC AG (SEQ ID NO: 210). PmpD was also expressed as two overlapping proteins. The pmpD-amino terminal portion, which lacks the signal sequence, (SEQ ID NO: 185, with the corresponding amino acid sequence provided in SEQ ID NO: 193) contains the initiating codon of the pET17b and is expressed as a 80 kD protein. For protein expression and purification purposes, a six-histidine tag follows the initiation codon and is fused at the 28th amino acid (nucleotide 84) of the gene. The following primers were used, 5' oligo, CAG ACA TAT GCA TCA CCA TCA CCA TCA CGG GTT AGC (SEQ ID NO: 211), and the 3' oligo- CAG AGG TAC CTC AGC TCC TCC AGC ACA CTC TCT TC (SEQ ID NO: 212), to splice into the 5' NdeI/3' KPN cloning site of the vector. The pmpD-carboxy terminus portion (SEQ ID NO: 184) was expressed as a 92 kD protein (SEQ ID NO: 192). For expression and subsequent purification, an additional methionine, alanine and serine was included, which represent the initiation codon and the first two amino acids from the pET17b vector. A six-histidine tag downstream of the methionine, alanine and serine is fused at the 691st amino acid (nucleotide 2073) of the gene. The 5' oligo- CAG AGC TAG CCA TCA CCA TCA CCA TCA CGG TGC TAT TTC TTG CTT ACG TGG (SEQ ID NO: 213) and the 3' oligo- CAG AGG TAC TTn AAA AGA TCA ATC GCA ATC CAG TAT TCG (SEQ ID NO: 214) were used to subclone the insert into the 5' NheI/3' KPN cloning site of the expression vector. PmpE was expressed as a 106kD protein (SEQ ID NO: 183 with the corresponding amino acid sequence provided in SEQ ID NO: 191). The pmpE insert also lacks the native signal sequence. PCR amplification of the gene under conditions well known in the art was performed using

the following oligo primers: 5' oligo- CAG AGG ATC CAC ATC ACC ATC ACC ATC ACG GAC TAG CTA GAG AGG TTC (SEQ ID NO: 215), and the 3' oligo- CAG AGA ATT CCT AGA ATC GCA GAG CAA TTT C (SEQ ID NO: 216), and the amplified insert was ligated into a 5' BamHI/3' EcoRI site of JA4304. The short
 5 nucleotide sequence, as provided in SEQ ID NO: 217, was inserted upstream of the initiation codon for creating the Kozak-like sequence and reconstituting the HindIII site. The expressed protein contains the initiation codon and the downstream 21 amino acids from the pET17b expression vector, i.e., MASMTGGQQMGRDSSLVPSSDP (SEQ ID NO: 218). In addition, a six-histidine tag is included upstream of the sequence
 10 described above and is fused at the 28th amino acid (nucleotide 84) of the gene, which eliminates the hypothetical signal peptide. The sequences provided in SEQ ID NO: 183 with the corresponding amino acid sequence provided in SEQ ID NO: 191 do not include these additional sequences. The pmpG gene (SEQ ID NO: 182, with the corresponding amino acid sequence provided in SEQ ID No; 190) was PCR amplified
 15 under conditions well known in the art using the following oligo primers: 5' oligo- CAG AGG TAC CGC ATC ACC ATC ACC ATC ACA TGA TTC CTC AAG GAA TTT ACG (SEQ ID NO: 219), and the 3' oligo- CAG AGC GGC CGC TTA GAA CCG GAC TTT ACT TCC (SEQ ID NO: 220), and ligated into the 5' KPN/3' NotI cloning site of the expression vector. The expressed protein contains an additional
 20 amino acid sequence at the amino end, namely, MASMTGGQQNGRDSSLVPHHHHHH (SEQ ID NO: 221), which comprises the initiation codon and additional sequence from the pET17b expression vector. The pmpl gene (SEQ ID NO: 181, with the corresponding amino acid sequence provided in SEQ ID No; 189) was PCR amplified under conditions well known in the art using the
 25 following oligo primers: 5' oligo- CAG AGC TAG CCA TCA CCA TCA CCA TCA CCT CTT TGG CCA GGA TCC C (SEQ ID NO: 222), and the 3' oligo- CAG AAC TAG TCT AGA ACC TGT AAG TGG TCC (SEQ ID NO: 223), and ligated into the expression vector at the 5' NheI/3' SpeI cloning site. The 95 kD expressed protein contains the initiation codon plus an additional alanine and serine from the pET17b
 30 vector at the amino end of the protein. In addition, a six-histidine tag is fused at the 21st amino acid of the gene, which eliminates the hypothetical signal peptide.

Clone 14H1-4, (SEQ ID NO: 56), identified using the TCT-3 cell line, contains a complete ORF for the TSA gene, thiol specific antioxidant - CT603 (the CT603 ORF is a homolog of CPn0778 from *C. pneumoniae*). The TSA open reading
 35 frame in clone 14-H1-4 was amplified such that the expressed protein possess an additional methionine and a 6x histidine tag (amino terminal end). This amplified insert

was sub-cloned into the Nde/EcoRI sites of the pET17b vector. Upon induction of this clone with IPTG, a 22.6 kDa protein was purified by Ni-NTA agarose affinity chromatography. The determined amino acid sequence for the 195 amino acid ORF of clone 14-H1-4 encoding the TSA gene is provided in SEQ ID NO: 65. Further analysis yielded a full-length clone for the TSA gene, referred to as CTL2-TSA-FL, with the full-length amino acid sequence provided in SEQ ID NO: 92.

Further studies yielded 10 additional clones identified by the TCT-1 and TCT-3 T-cell lines, as described above. The clones identified by the TCT-1 line are: 16-D4-22, 17-C5-19, 18-C5-2, 20-G3-45 and 21-C7-66; clones identified by the TCT-3 cell line are: 17-C10-31, 17-E2-9, 22-A1-49 and 22-B3-53. Clone 21-G12-60 was recognized by both the TCT-1 and TCT-3 T cell lines. Clone 16-D4-22 (SEQ ID NO: 119), identified using the TCT-1 cell line contains a 953 bp insert that contains two genes, parts of open reading frame 3 (ORF3) and ORF4 of the *C. trachomatis* plasmid for growth within mammalian cells. Clone 17-C5-19 (SEQ ID NO: 118), contains a 951 bp insert that contains part of the ORF for DT431, encoding for clpP_1 protease and part of the ORF for CT430 (diaminopimelate epimerase). Clone 18-C5-2 (SEQ ID NO: 117) is part of the ORF for S1 ribosomal protein with a 446 bp insert that was identified using the TCT-1 cell line. Clone 20-G3-45 (SEQ ID NO: 116), identified by the TCT-1 cell line, contains a 437 bp insert that is part of the pmpB gene (CT413). Clone 21-C7-66 (SEQ ID NO: 115), identified by the TCT-1 line, contains a 995bp insert that encodes part of the dnaK like protein. The insert of this clone does not overlap with the insert of the TCT-3 clone 11-H4-28 (SEQ ID NO: 59), which was shown to be part of the dnaK gene CT396. Clone 17-C10-31 (SEQ ID NO: 114), identified by the TCT-3 cell line, contains a 976 bp insert. This clone contains part of the ORF for CT858, a protease containing IRBP and DHR domains. Clone 17-E2-9 (SEQ ID NO: 113) contains part of ORFs for two genes, CT611 and CT610, that span a 1142 bp insert. Clone 22-A1-49 (SEQ ID NO: 112), identified using the TCT-3 line, also contains two genes in a 698 bp insert. Part of the ORF for CT660 (DNA gyrase{gyrA_2}) is present on the top strand where as the complete ORF for a hypothetical protein CT659 is present on the complementary strand. Clone 22-B3-53 (SEQ ID NO: 111), identified by the TCT-1 line, has a 267 bp insert that encodes part of the ORF for GroEL (CT110). Clone 21-G12-60 (SEQ ID NO: 110), identified by both the TCT-1 and TCT-3 cell lines contains a 1461 bp insert that contains partial ORFs for hypothetical proteins CT875, CT229 and CT228.

Additional *Chlamydia* antigens were obtained by screening a genomic expression library of *Chlamydia trachomatis* (LGV II serovar) in Lambda Screen-1

vector (Novagen, Madison, WI) with sera pooled from several *Chlamydia*-infected individuals using techniques well known in the art. The following immuno-reactive clones were identified and the inserts containing *Chlamydia* genes sequenced: CTL2#1 (SEQ ID NO: 71); CTL2#2 (SEQ ID NO: 70); CTL2#3-5' (SEQ ID NO: 72, a first
 5 determined genomic sequence representing the 5' end); CTL2#3-3' (SEQ ID NO: 73, a second determined genomic sequence representing the 3' end); CTL2#4 (SEQ ID NO: 53); CTL2#5 (SEQ ID NO: 69); CTL2#6 (SEQ ID NO: 68); CTL2#7 (SEQ ID NO: 67); CTL2#8b (SEQ ID NO: 54); CTL2#9 (SEQ ID NO: 66); CTL2#10-5' (SEQ ID NO: 74, a first determined genomic sequence representing the 5' end); CTL2#10-3' (SEQ ID
 10 NO: 75, a second determined genomic sequence representing the 3' end); CTL2#11-5' (SEQ ID NO: 45, a first determined genomic sequence representing the 5' end); CTL2#11-3' (SEQ ID NO: 44, a second determined genomic sequence representing the 3' end); CTL2#12 (SEQ ID NO: 46); CTL2#16-5' (SEQ ID NO: 47); CTL2#18-5' (SEQ ID NO: 49, a first determined genomic sequence representing the 5' end);
 15 CTL2#18-3' (SEQ ID NO: 48, a second determined genomic sequence representing the 3' end); CTL2#19-5' (SEQ ID NO: 76, the determined genomic sequence representing the 5' end); CTL2#21 (SEQ ID NO: 50); CTL2#23 (SEQ ID NO: 51; and CTL2#24 (SEQ ID NO: 52).

Additional *Chlamydia trachomatis* antigens were identified by
 20 serological expression cloning. These studies used sera pooled from several *Chlamydia*-infected individuals, as described above, but, IgA, and IgM antibodies were used in addition to IgG as a secondary antibody. Clones screened by this method enhance detection of antigens recognized by an early immune response to a *Chlamydial* infection, that is a mucosal humoral immune response. The following immunoreactive
 25 clones were characterized and the inserts containing *Chlamydia* genes sequenced: CTL2gam-1 (SEQ ID NO: 290), CTL2gam-2 (SEQ ID NO: 289), CTL2gam-5 (SEQ ID NO: 288), CTL2gam-6-3' (SEQ ID NO: 287, a second determined genomic sequence representing the 3' end), CTL2gam-6-5' (SEQ ID NO: 286, a first determined genomic sequence representing the 5' end), CTL2gam-8 (SEQ ID NO: 285), CTL2gam-10 (SEQ
 30 ID NO: 284), CTL2gam-13 (SEQ ID NO: 283), CTL2gam-15-3' (SEQ ID NO: 282, a second determined genomic sequence representing the 3' end), CTL2gam-15-5' (SEQ ID NO: 281, a first determined genomic sequence representing the 5' end), CTL2gam-17 (SEQ ID NO: 280), CTL2gam-18 (SEQ ID NO: 279), CTL2gam-21 (SEQ ID NO: 278), CTL2gam-23 (SEQ ID NO: 277), CTL2gam-24 (SEQ ID NO: 276), CTL2gam-26
 35 (SEQ ID NO: 275), CTL2gam-27 (SEQ ID NO: 274), CTL2gam-28 (SEQ ID NO: 273), CTL2gam-30-3' (SEQ ID NO: 272, a second determined genomic sequence

representing the 3' end) and CTL2gam-30-5' (SEQ ID NO: 271, a first determined genomic sequence representing the 5' end).

EXAMPLE 2

5 INDUCTION OF T CELL PROLIFERATION AND INTERFERON- γ PRODUCTION BY *CHLAMYDIA TRACHOMATIS* ANTIGENS

The ability of recombinant *Chlamydia trachomatis* antigens to induce T cell proliferation and interferon- γ production is determined as follows.

Proteins are induced by IPTG and purified by Ni-NTA agarose affinity
10 chromatograph (Webb et al., *J. Immunology* 157:5034-5041, 1996). The purified polypeptides are then screened for the ability to induce T-cell proliferation in PBMC preparations. PBMCs from *C. trachomatis* patients as well as from normal donors whose T-cells are known to proliferate in response to *Chlamydia* antigens, are cultured in medium comprising RPMI 1640 supplemented with 10% pooled human serum and
15 50 μ g/ml gentamicin. Purified polypeptides are added in duplicate at concentrations of 0.5 to 10 μ g/mL. After six days of culture in 96-well round-bottom plates in a volume of 200 μ l, 50 μ l of medium is removed from each well for determination of IFN- γ levels, as described below. The plates are then pulsed with 1 μ Ci/well of tritiated thymidine for a further 18 hours, harvested and tritium uptake determined using a gas
20 scintillation counter. Fractions that result in proliferation in both replicates three fold greater than the proliferation observed in cells cultured in medium alone are considered positive.

IFN- γ is measured using an enzyme-linked immunosorbent assay (ELISA). ELISA plates are coated with a mouse monoclonal antibody directed to
25 human IFN- γ (PharMingen, San Diego, CA) in PBS for four hours at room temperature. Wells are then blocked with PBS containing 5% (W/V) non-fat dried milk for 1 hour at room temperature. The plates are washed six times in PBS/0.2% TWEEN-20 and samples diluted 1:2 in culture medium in the ELISA plates are incubated overnight at room temperature. The plates are again washed and a polyclonal rabbit anti-human
30 IFN- γ serum diluted 1:3000 in PBS/10% normal goat serum is added to each well. The plates are then incubated for two hours at room temperature, washed and horseradish peroxidase-coupled anti-rabbit IgG (Sigma Chemical So., St. Louis, MO) is added at a 1:2000 dilution in PBS/5% non-fat dried milk. After a further two hour incubation at room temperature, the plates are washed and TMB substrate added. The reaction is
35 stopped after 20 min with 1 N sulfuric acid. Optical density is determined at 450 nm using 570 nm as a reference wavelength. Fractions that result in both replicates giving

an OD two fold greater than the mean OD from cells cultured in medium alone, plus 3 standard deviations, are considered positive.

Using the above methodology, recombinant 1B1-66 protein (SEQ ID NO: 5) as well as two synthetic peptides corresponding to amino acid residues 48-67 (SEQ ID NO: 13; referred to as 1-B1-66/48-67) and 58-77 (SEQ ID NO: 14, referred to as 1B1-66/58-77), respectively, of SEQ ID NO: 5, were found to induce a proliferative response and IFN- γ production in a Chlamydia-specific T cell line used to screen a genomic library of *C. trachomatis* LGV II.

Further studies have identified a *C. trachomatis*-specific T-cell epitope in the ribosomal S13 protein. Employing standard epitope mapping techniques well known in the art, two T-cell epitopes in the ribosomal S13 protein (rS13) were identified with a *Chlamydia*-specific T-cell line from donor CL-8 (T-cell line TCL-8 EB/DC). Fig. 8 illustrates that the first peptide, rS13 1-20 (SEQ ID NO: 106), is 100% identical with the corresponding *C. pneumoniae* sequence, explaining the cross-reactivity of the T-cell line to recombinant *C. trachomatis*- and *C. pneumoniae*-rS13. The response to the second peptide rS13 56-75 (SEQ ID NO: 108) is *C. trachomatis*-specific, indicating that the rS13 response in this healthy asymptomatic donor was elicited by exposure to *C. trachomatis* and not to *C. pneumoniae*, or any other microbial infection.

As described in Example 1, Clone 11-C12-91 (SEQ ID NO: 63), identified using the TCP-21 cell line, has a 269 bp insert that is part of the OMP2 gene (CT443) and shares homology with the 60 kDa cysteine rich outer membrane protein of *C. pneumoniae*, referred to as OMCB. To further define the reactive epitope(s), epitope mapping was performed using a series of overlapping peptides and the immunoassay previously described. Briefly, proliferative responses were determined by stimulating 2.5×10^4 TCP-21 T-cells in the presence of 1×10^6 monocyte-derived dendritic cells with either non-infectious elementary bodies derived from *C. trachomatis* and *C. pneumoniae*, or peptides derived from the protein sequence of *C. trachomatis* or *C. pneumoniae* OMCB protein (0.1 μ g/ml). The TCP-21 T-cells responded to epitopes CT-OMCB #167-186, CT-OMCB #171-190, CT-OMCB #171-186, and to a lesser extent, CT-OMCB #175-186 (SEQ ID NO: 249-252, respectively). Notably, the TCP-21 T-cell line also gave a proliferative response to the homologous *C. pneumoniae* peptide CP-OMCB #171-186 (SEQ ID NO: 253), which was equal to or greater than the response to the *C. trachomatis* peptides. The amino acid substitutions in position two (i.e., Asp for Glu) and position four (i.e., Cys for Ser) did not alter the proliferative

response of the T-cells and therefore demonstrating this epitope to be a cross-reactive epitope between *C. trachomatis* and *C. pneumoniae*.

To further define the epitope described above, an additional T-cell line, TCT-3, was used in epitope mapping experiments. The immunoassays were performed as described above, except that only peptides from *C. trachomatis* were tested. The T-cells gave a proliferative response to two peptides, CT-OMCB #152-171 and CT-OMCB #157-176 (SEQ ID NO: 246 and 247, respectively), thereby defining an additional immunogenic epitope in the cysteine rich outer membrane protein of *C. trachomatis*.

Clone 14H1-4, (SEQ ID NO: 56, with the corresponding full-length amino acid sequence provided in SEQ ID NO: 92), was identified using the TCT-3 cell line in the CD4 T-cell expression cloning system previously described, and was shown to contain a complete ORF for the, thiol specific antioxidant gene (CT603), referred to as TSA. Epitope mapping immunoassays were performed, as described above, to further define the epitope. The TCT-3 T-cells line exhibited a strong proliferative response to the overlapping peptides CT-TSA #96-115, CT-TSA #101-120 and CT-TSA #106-125 (SEQ ID NO: 254-256, respectively) demonstrating an immunoreactive epitope in the thiol specific antioxidant gene of *C. trachomatis* serovar LGVII.

EXAMPLE 3

PREPARATION OF SYNTHETIC POLYPEPTIDES

Polypeptides may be synthesized on a Millipore 9050 peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugating or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray mass spectrometry and by amino acid analysis.

EXAMPLE 4

ISOLATION AND CHARACTERIZATION OF DNA SEQUENCES ENCODING
CHLAMYDIA ANTIGENS USING RETROVIRAL EXPRESSION VECTOR SYSTEMS
AND SUBSEQUENT IMMUNOLOGICAL ANALYSIS

5 A genomic library of *Chlamydia trachomatis* LGV II was constructed by limited digests using BamHI, BglII, BstYI and MboI restriction enzymes. The restriction digest fragments were subsequently ligated into the BamHI site of the retroviral vectors pBIB-KS1,2,3. This vector set was modified to contain a Kosak
10 translation initiation site and stop codons in order to allow expression of proteins from short DNA genomic fragments, as shown in Fig. 2. DNA pools of 80 clones were prepared and transfected into the retroviral packaging line Phoenix-Ampho, as described in Pear, W.S., Scott, M.L. and Nolan, G.P., Generation of High Titre, Helper-free Retroviruses by Transient Transfection. Methods in Molecular Medicine: Gene
15 Therapy Protocols, Humana Press, Totowa, NJ, pp. 41-57. The *Chlamydia* library in retroviral form was then transduced into H2-Ld expressing P815 cells, which were then used as target cells to stimulate an antigen specific T-cell line.

A *Chlamydia*-specific, murine H2^d restricted CD8⁺ T-cell line was expanded in culture by repeated rounds of stimulation with irradiated *C. trachomatis*-
20 infected J774 cells and irradiated syngeneic spleen cells, as described by Starnbach, M., in *J. Immunol.*, 153:5183, 1994. This *Chlamydia*-specific T-cell line was used to screen the above *Chlamydia* genomic library expressed by the retrovirally-transduced P815 cells. Positive DNA pools were identified by detection of IFN- γ production using Elispot analysis (see Lalvani et al., *J. Experimental Medicine* 186:859-865, 1997).

25 Two positive pools, referred to as 2C7 and 2E10, were identified by IFN- γ Elispot assays. Stable transductants of P815 cells from pool 2C7 were cloned by limiting dilution and individual clones were selected based upon their capacity to elicit IFN- γ production from the *Chlamydia*-specific CTL line. From this screening process, four positive clones were selected, referred to as 2C7-8, 2C7-9, 2C7-19 and 2C7-21.
30 Similarly, the positive pool 2E10 was further screened, resulting in an additional positive clone, which contains three inserts. The three inserts are fragments of the CT016, tRNA synthase and clpX genes (SEQ ID NO: 268-270, respectively).

Transgenic DNA from these four positive 2C7 clones were PCR amplified using pBIB-KS specific primers to selectively amplify the *Chlamydia* DNA
35 insert. Amplified inserts were gel purified and sequenced. One immunoreactive clone, 2C7-8 (SEQ ID NO: 15, with the predicted amino acid sequence provided in SEQ ID

NO: 32), is a 160 bp fragment with homology to nucleotides 597304-597145 of *Chlamydia trachomatis*, serovar D (NCBI, BLASTN search; SEQ ID NO: 33, with the predicted amino acid sequence provided in SEQ ID NO: 34). The sequence of clone 2C7-8 maps within two putative open reading frames from the region of high homology described immediately above, and in particular, one of these putative open reading frames, consisting of a 298 amino acid fragment (SEQ ID NO: 16, with the predicted amino acid sequence provided in SEQ ID NO: 17), was demonstrated to exhibit immunological activity.

Full-length cloning of the 298 amino acid fragment (referred to as CT529 and/or the Cap1 gene) from serovar L2 was obtained by PCR amplification using 5'-ttttgaagcaggtaggatgaatg (forward) (SEQ ID NO: 159) and 5'-ttaagaaatttaaaatccctta (reverse) (SEQ ID NO: 160) primers, using purified *C. trachomatis* L2 genomic DNA as template. This PCR product was gel-purified, cloned into pCRblunt (Invitrogen, Carlsbad, CA) for sequencing, and then subcloned into the EcoRI site of pBIB-KMS, a derivative of pBIB-KS for expression. The *Chlamydia pneumoniae* homologue of CT529 is provided in SEQ ID NO: 291, with the corresponding amino acid sequence provided in SEQ ID NO: 292.

Full-length DNA encoding various CT529 serovars were amplified by PCR from bacterial lysates containing 10^5 IFU, essentially as described (Denamur, E., C. Sayada, A. Souriau, J. Orfila, A. Rodolakis and J. Elion. 1991. J. Gen. Microbiol. 137: 2525). The following serovars were amplified as described: Ba (SEQ ID NO: 134, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 135); E (BOUR) and E (MTW447) (SEQ ID NO: 122, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 123); F (NI1) (SEQ ID NO: 128, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 129); G; (SEQ ID NO: 126, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 127); Ia (SEQ ID NO: 124, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 125); L1 (SEQ ID NO: 130, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 131); L3 (SEQ ID NO: 132, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 133); I (SEQ ID NO: 263, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 264); K (SEQ ID NO: 265, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 266); and MoPn (SEQ ID NO: 136, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 137). PCR reactions were performed with Advantage Genomic PCR Kit (Clontech, Palo Alto, CA) using primers specific for serovar L2 DNA (external to the ORF). Primers sequences were 5'-

gggtataatctctctaaatttg (forward-SEQ ID NO: 161) and 5'-agataaaaaaggctgttc' (reverse-SEQ ID NO: 162) except for MoPn which required 5'-ttttgaagcaggtaggtgaatatg (forward-SEQ ID NO: 163) and 5'-tttaacaataagaaaagctaagcactttgt (reverse-SEQ ID NO: 164). PCR amplified DNA was purified with QIAquick PCR purification kit (Qiagen, Valencia, CA) and cloned in pCR2.1 (Invitrogen, Carlsbad, CA) for sequencing.

Sequencing of DNA derived from PCR amplified inserts of immunoreactive clones was done on an automated sequencer (ABI 377) using both a pBIB-KS specific forward primer 5'-ccttacacagtctgtgac (SEQ ID NO: 165) and a reverse primer 3'-gtttccggggccctcacattg (SEQ ID NO: 166). PCRBlunt cloned DNA coding for CT529 serovar L2 and pCR2.1 cloned DNA coding for CT529 serovar Ba, E (BOUR), E (MTW447), F (NI1), G, Ia, K, L1, L3 and MoPn were sequenced using T7 promoter primer and universal M13 forward and M13 reverse primers.

To determine if these two putative open reading frames (SEQ ID NO: 16 and 20) encoded a protein with an associated immunological function, overlapping peptides (17-20 amino acid lengths) spanning the lengths of the two open reading frames were synthesized, as described in Example 3. A standard chromium release assay was utilized to determine the per cent specific lysis of peptide-pulsed H2^d restricted target cells. In this assay, aliquots of P815 cells (H2^d) were labeled at 37° C for one hour with 100 µCi of ⁵¹Cr in the presence or absence of 1 µg/ml of the indicated peptides. Following this incubation, labeled P815 cells were washed to remove excess ⁵¹Cr and peptide, and subsequently plated in duplicate in microculture plates at a concentration of 1,000 cells/well. Effector CTL (*Chlamydia*-specific CD8 T cells) were added at the indicated effector:target ratios. Following a 4 hour incubation, supernatants were harvested and measured by gamma-counter for release of ⁵¹Cr into the supernatant. Two overlapping peptides from the 298 amino acid open reading frame did specifically stimulate the CTL line. The peptides represented in SEQ ID NO: 138-156 were synthesized, representing the translation of the L2 homologue of the serovar D open reading frame for CT529 (Cap1 gene) and 216 amino acid open reading frame. As shown in Fig. 3, peptides CtC7.8-12 (SEQ ID NO: 18, also referred to as Cap1#132-147, SEQ ID NO: 139) and CtC7.8-13 (SEQ ID NO: 19, also referred to as Cap1#138-155, SEQ ID NO: 140) were able to elicit 38 to 52% specific lysis, respectively, at an effector to target ratio of 10:1. Notably, the overlap between these two peptides contained a predicted H2^d (K^d and L^d) binding peptide. A 10 amino acid peptide was synthesized to correspond to this overlapping sequence (SEQ ID NO: 31) and was found to generate a strong immune response from the anti-*Chlamydia* CTL line by elispot assay. Significantly, a search of the most recent Genbank database revealed no

proteins have previously been described for this gene. Therefore, the putative open reading frame encoding clone 2C7-8 (SEQ ID NO: 15) defines a gene which encompasses an antigen from *Chlamydia* capable of stimulating antigen-specific CD8+ T-cells in a MHC-I restricted manner, demonstrating this antigen could be used to
5 develop a vaccine against *Chlamydia*.

To confirm these results and to further map the epitope, truncated peptides (SEQ ID NO: 138-156) were made and tested for recognition by the T-cells in an IFN- γ ELISPOT assay. Truncations of either Ser139 (Cap1#140-147, SEQ ID NO: 146) or Leu147 (Cap1#138-146, SEQ ID NO: 147) abrogate T-cell recognition. These
10 results indicate that the 9-mer peptide Cap1#139-147 (SFIGGITYL, SEQ ID NO: 145) is the minimal epitope recognized by the *Chlamydia*-specific T-cells.

Sequence alignments of Cap1 (CT529) from selected serovars of *C. trachomatis* (SEQ ID NO: 121, 123, 125, 127, 129, 131, 133, 135, 137 and 139) shows one of the amino acid differences is found in position 2 of the proposed epitope. The
15 homologous serovar D peptide is SIIGGITYL (SEQ ID NO: 168). The ability of SFIGGITYL and SIIGGITYL to target cells for recognition by the *Chlamydia* specific T-cells was compared. Serial dilutions of each peptide were incubated with P815 cells and tested for recognition by the T-cells in a ^{51}Cr release assay, as described above. The *Chlamydia*-specific T-cells recognize the serovar L2 peptide at a minimum
20 concentration of 1 nM and the serovar D peptide at a minimum concentration of 10 nM.

Further studies have shown that a Cap1#139-147-specific T-cell clone recognizes *C. trachomatis* infected cells. To confirm that Cap1₁₃₉₋₁₄₇ is presented on the surface of *Chlamydia* infected cells, Balb-3T3 (H-2^d) cells were infected with *C. trachomatis* serovar L2 and tested to determine whether these cells are recognized by a
25 CD8+ T-cell clone specific for Cap1#139-147 epitope (SEQ ID NO: 145). The T-cell clone specific for Cap1#139-147 epitope was obtained by limiting dilution of the line 69 T-cells. The T-cell clone specifically recognized the *Chlamydia* infected cells. In these experiments, target cells were *C. trachomatis* infected (positive control) or uninfected Balb/3T3 cells, showing 45%, 36% and 30% specific lysis at 30:1, 10:1 and
30 3:1 effector to target ratios, respectively; or Cap1#139-147 epitope (SEQ ID NO: 145) coated, or untreated P815 cells, showing 83%, 75% and 58% specific lysis at 30:1, 10:1 and 3:1 effector to target ratios, respectively (negative controls having less than 5% lysis in all cases). This data suggests that the epitope is presented during infection.

In vivo studies show Cap1#139-147 epitope-specific T-cells are primed
35 during murine infection with *C. trachomatis*. To determine if infection with *C. trachomatis* primes a Cap1#139-147 epitope-specific T-cell response, mice were

infected i.p. with 10^8 IFU of *C. trachomatis* serovar L2. Two weeks after infection, the mice were sacrificed and spleen cells were stimulated on irradiated syngeneic spleen cells pulsed with Cap1#139-147 epitope peptide. After 5 days of stimulation, the cultures were used in a standard ^{51}Cr release assay to determine if there were Cap1#139-147 epitope-specific T-cells present in the culture. Specifically, spleen cells from a *C. trachomatis* serovar L2 immunized mouse or a control mouse injected with PBS after a 5 days culture with Cap1#139-147 peptide-coated syngeneic spleen cells and CD8⁺ T-cells able to specifically recognize Cap1#139-147 epitope gave 73%, 60% and 32% specific lysis at a30:1, 10:1 and 3:1 effector to target ratios, respectively. The control mice had a percent lysis of approximately 10% at a 30:1 effector to target ratio, and steadily declining with lowering E:T ratios. Target cells were Cap1#139-147 peptide-coated, or untreated P815 cells. These data suggest that Cap1#139-147 peptide-specific T-cells are primed during murine infection with *C. trachomatis*.

Studies were performed demonstrating that Ct529 (referred to herein as Cap-1) localizes to the inclusion membrane of *C. trachomatis*-infected cells and is not associated with elementary bodies or reticulate bodies. As described above, Cap-1 was identified as a product from *Chlamydia* that stimulates CD8⁺ CTL. These CTL are protective in a murine model of infection, thus making Cap-1 a good vaccine candidate. Further, since these CTL are MHC-I restricted, the Cap-1 gene must have access to the cytosol of infected cells, which may be a unique characteristic of specific *Chlamydial* gene products. Therefore, determination of the cellular localization of the gene products would be useful in characterizing Cap-1 as a vaccine candidate. To detect the intracellular localization of Cap-1, rabbit polyclonal antibodies directed against a recombinant polypeptide encompassing the N-terminal 125 amino acids of Cap-1 (SEQ ID NO: 305, with the amino acid sequence including the N-terminal 6-His tag provided in SEQ ID NO: 304) were used to stain McCoy cells infected with *Chlamydiae*.

Rabbit-anti-Cap-1 polyclonal antibodies were obtained by hyperimmunization of rabbits with a recombinant polypeptide, rCt529c1-125 (SEQ ID NO: 305) encompassing the N-terminal portion of Cap-1. Recombinant rCt529c1-125 protein was obtained from *E. coli* transformed with a pET expression plasmid (as described above) encoding the nucleotides 1-375 encoding the N-terminal 1-125 amino acids of Cap-1. Recombinant protein was purified by Ni-NTA using techniques well known in the art. For a positive control antiserum, polyclonal antisera directed against elementary bodies were made by immunization of rabbits with purified *C. trachomatis* elementary bodies (Biodesign, Sacco, Maine). Pre-immune sera derived from rabbits prior to immunization with the Cap-1 polypeptide was used as a negative control.

Immunocytochemistry was performed on McCoy cell monolayers grown on glass coverslips inoculated with either *C. trachomatis* serovar L2 or *C. psittaci*, strain 6BC, at a concentration of 10^6 IFU (Inclusion Forming Units) per ml. After 2 hours, medium was aspirated and replaced with fresh RP-10 medium supplemented with cycloheximide (1.0 μ g/ml). Infected cells were incubated at in 7% CO₂ for 24 hours and fixed by aspirating medium, rinsing cells once with PBS and methanol fixation for 5 minutes. For antigen staining, fixed cell monolayers were washed with PBS and incubated at 37°C for 2 hours with 1:100 dilutions of specific or control antisera. Cells were rinsed with PBS and incubated for 1 hour with fluorescein isothiocyanate (FITC)-labeled, anti-rabbit IgG (KPL, Gaithersburg) and stained with Evans blue (0.05%) in PBS. Fluorescence was observed with a 100X objective (Zeiss epifluorescence microscope), and photographed (Nikon UFX-11A camera).

Results from this study show Cap-1 localizes to the inclusion membrane of *C. trachomatis*-infected cells. Cap-1 specific antibody labeled the inclusion membranes of *C. trachomatis*-infected cells, but not *Chlamydial* elementary bodies contained in these inclusions or released by the fixation process. Conversely, the anti-elementary body antibody clearly labeled the bacterial bodies, not only within the inclusions, but those released by the fixation process. Specificity of the anti-Cap-1 antibody is demonstrated by the fact that it does not stain *C. psittaci*-infected cells. Specificity of the Cap-1 labeling is also shown by the absence of reactivity in pre-immune sera. These results suggest that Cap-1 is released from the bacteria and becomes associated with the *Chlamydial* inclusion membrane. Therefore, Cap-1 is a gene product which may be useful for stimulating CD8+ T cells in the development of a vaccine against infections caused by *Chlamydia*.

The relevance of the Cap-1 gene as a potential CTL antigen in a vaccine against *Chlamydia* infection is further illustrated by two additional series of studies. First, CTL specific for the MHC-I epitope of Cap-1 CT529 #138-147 peptide of *C. trachomatis* (SEQ ID NO: 144) have been shown to be primed to a high frequency during natural infection. Specifically, Balb/C mice were inoculated with 10^6 I.F.U. of *C. trachomatis*, serova L2. After 2 weeks, spleens were harvested and quantified by Elispot analysis for the number of IFN- γ secreting cells in response to Cap-1 #138-147 peptide-pulsed antigen presenting cells. In two experiments, the number of IFN- γ -secreting cells in 10^5 splenocytes was about 1% of all CD8+ T-cells. This high frequency of responding CD8+ CTL to the MHC-I epitope (Cap-1 CT529 #138-147 peptide) suggest that Cap-1 is highly immunogenic in infections.

Results from a second series of studies have shown that the Cap-1 protein is almost immediately accessible to the cytosol of the host cell upon infection. This is shown in a time-course of Cap-1 CT529 #138-147 peptide presentation. Briefly, 3T3 cells were infected with *C. trachomatis* serovar L2 for various lengths of time, and then tested for recognition by Cap-1 CT529 #138-147 peptide-specific CTL. The results show that *C. trachomatis*-infected 3T3 cells are targeted for recognition by the antigen-specific CTL after only 2 hours of infection. These results suggest that Cap-1 is an early protein synthesized in the development of *C. trachomatis* elementary bodies to reticulate bodies. A CD8+ CTL immune response directed against a gene product expressed early in infection may be particularly efficacious in a vaccine against *Chlamydia* infection.

EXAMPLE 5

GENERATION OF ANTIBODY AND T-CELL RESPONSES IN MICE IMMUNIZED WITH CHLAMYDIA ANTIGENS

Immunogenicity studies were conducted to determine the antibody and CD4+ T cell responses in mice immunized with either purified SWIB or S13 proteins formulated with Montanide adjuvant, or DNA-based immunizations with pcDNA-3 expression vectors containing the DNA sequences for SWIB or S13. SWIB is also referred to as clone 1-B1-66 (SEQ ID NO: 1, with the corresponding amino acid sequence provided in SEQ ID NO: 5), and S13 ribosomal protein is also referred to as clone 10-C10-31 (SEQ ID NO: 4, with the corresponding amino acid sequence provided in SEQ ID NO: 12). In the first experiment, groups of three C57BL/6 mice were immunized twice and monitored for antibody and CD4+ T-cell responses. DNA immunizations were intradermal at the base of the tail and polypeptide immunizations were administered by subcutaneous route. Results from standard ³H-incorporation assays of spleen cells from immunized mice shows a strong proliferative response from the group immunized with purified recombinant SWIB polypeptide (SEQ ID NO: 5). Further analysis by cytokine induction assays, as previously described, demonstrated that the group immunized with SWIB polypeptide produced a measurable IFN- γ and IL-4 response. Subsequent ELISA-based assays to determine the predominant antibody isotype response in the experimental group immunized with the SWIB polypeptide were performed. Fig. 4 illustrates the SWIB-immunized group gave a humoral response that was predominantly IgG1.

In a second experiment, C3H mice were immunized three times with 10 μ g purified SWIB protein (also referred to as clone 1-B1-66, SEQ ID NO: 5)

formulated in either PBS or Montanide at three week intervals and harvested two weeks after the third immunization. Antibody titers directed against the SWIB protein were determined by standard ELISA-based techniques well known in the art, demonstrating the SWIB protein formulated with Montanide adjuvant induced a strong humoral immune response. T-cell proliferative responses were determined by a XTT-based assay (Scudiero, et al, *Cancer Research*, 1988, 48:4827). As shown in Fig. 5, splenocytes from mice immunized with the SWIB polypeptide plus Montanide elicited an antigen specific proliferative response. In addition, the capacity of splenocytes from immunized animals to secrete IFN- γ in response to soluble recombinant SWIB polypeptide was determined using the cytokine induction assay previously described. The splenocytes from all animals in the group immunized with SWIB polypeptide formulated with montanide adjuvant secreted IFN- γ in response to exposure to the SWIB Chlamydia antigen, demonstrating an *Chlamydia*-specific immune response.

In a further experiment, C3H mice were immunized at three separate time points at the base of the tail with 10 μ g of purified SWIB or S13 protein (*C. trachomatis*, SWIB protein, clone 1-B1-66, SEQ ID NO: 5, and S13 protein, clone 10-C10-31, SEQ ID NO: 4) formulated with the SBAS2 adjuvant (SmithKline Beecham, London, England). Antigen-specific antibody titers were measured by ELISA, showing both polypeptides induced a strong IgG response, ranging in titers from 1×10^4 to 1×10^5 . The IgG1 and IgG2a components of this response were present in fairly equal amounts. Antigen-specific T-cell proliferative responses, determined by standard 3 H-incorporation assays on spleen cells isolated from immunized mice, were quite strong for SWIB (50,000 cpm above the negative control) and even stronger for S13 (100,000 cpm above the negative control). The IFN γ production was assayed by standard ELISA techniques from supernatant from the proliferating culture. *In vitro* restimulation of the culture with S13 protein induced high levels of IFN γ production, approximately 25 ng/ml versus 2 ng/ml for the negative control. Restimulation with the SWIB protein also induced IFN γ , although to a lesser extent.

In a related experiment, C3H mice were immunized at three separate time points with 10 μ g of purified SWIB or S13 protein (*C. trachomatis*, SWIB protein, clone 1-B1-66, SEQ ID NO: 5, and S13 protein, clone 10-C10-31, SEQ ID NO: 4) mixed with 10 μ g of Cholera Toxin. Mucosal immunization was through intranasal inoculation. Antigen-specific antibody responses were determined by standard ELISA techniques. Antigen-specific IgG antibodies were present in the blood of SWIB-immunized mice, with titers ranging from 1×10^3 to 1×10^4 , but non-detectable in the S13-immunized animals. Antigen-specific T-cell responses from isolated splenocytes,

as measured by IFN γ production, gave similar results to those described immediately above for systemic immunization.

An animal study was conducted to determine the immunogenicity of the CT529 serovar LGVII CTL epitope, defined by the CT529 10mer consensus peptide (CSFIGGITYL – SEQ ID NO: 31), which was identified as an H2-Kd restricted CTL epitope. BALB/c mice (3 mice per group) were immunized three times with 25 μ g of peptide combined with various adjuvants. The peptide was administered systemically at the base of the tail in either SKB Adjuvant System SBAS-2", SBAS-7 (SmithKline Beecham, London, England) or Montanide. The peptide was also administered intranasally mixed with 10ug of Cholera Toxin (CT). Naive mice were used as a control. Four weeks after the 3rd immunization, spleen cells were restimulated with LPS-blasts pulsed with 10ug/ml CT529 10mer consensus peptide at three different effector to LPS-blasts ratios : 6, 1.5 and 0.4 at 1×10^6 cell/ml. After 2 restimulations, effector cells were tested for their ability to lyse peptide pulsed P815 cells using a standard chromium release assay. A non-relevant peptide from chicken egg ovalbumin was used as a negative control. The results demonstrate that a significant immune response was elicited towards the CT529 10mer consensus peptide and that antigen-specific T-cells capable of lysing peptide-pulsed targets were elicited in response to immunization with the peptide. Specifically, antigen-specific lytic activities were found in the SBAS-7 and CT adjuvanted group while Montanide and SBAS-2" failed to adjuvant the CTL epitope immunization.

EXAMPLE 6

EXPRESSION AND CHARACTERIZATION OF *CHLAMYDIA PNEUMONIAE* GENES

The human T-cell line, TCL-8, described in Example 1, recognizes *Chlamydia trachomatis* as well as *Chlamydia pneumonia* infected monocyte-derived dendritic cells, suggesting *Chlamydia trachomatis* and *pneumonia* may encode cross-reactive T-cell epitopes. To isolate the *Chlamydia pneumonia* genes homologous to *Chlamydia trachomatis* LGV II clones 1B1-66, also referred to as SWIB (SEQ ID NO: 1) and clone 10C10-31, also referred to as S13 ribosomal protein (SEQ ID NO: 4), HeLa 229 cells were infected with *C. pneumonia* strain TWAR (CDC/CWL-029). After three days incubation, the *C. pneumonia*-infected HeLa cells were harvested, washed and resuspended in 200 μ l water and heated in a boiling water bath for 20 minutes. Ten microliters of the disrupted cell suspension was used as the PCR template. *C. pneumonia* specific primers were designed for clones 1B1-66 and 10C10-31 such that the 5' end had a 6X-Histidine tag and a Nde I site inserted, and the

3' end had a stop codon and a BamHI site included (Fig. 6). The PCR products were amplified and sequenced by standard techniques well known in the art. The *C. pneumonia*-specific PCR products were cloned into expression vector pET17B (Novagen, Madison, WI) and transfected into *E. coli* BL21 pLysS for expression and subsequent purification utilizing the histidine-nickel chromatographic methodology provided by Novagen. Two proteins from *C. pneumonia* were thus generated, a 10-11 kDa protein referred to as CpSWIB (SEQ ID NO: 27, and SEQ ID NO: 78 having a 6X His tag, with the corresponding amino acid sequence provided in SEQ ID NO: 28, respectively), a 15 kDa protein referred to as CpS13 (SEQ ID NO: 29, and SEQ ID NO: 77, having a 6X His tag, with the corresponding amino acid sequence provided in SEQ ID NO: 30 and 91, respectively).

EXAMPLE 7

INDUCTION OF T CELL PROLIFERATION AND INTERFERON- γ PRODUCTION BY *CHLAMYDIA PNEUMONIAE* ANTIGENS

The ability of recombinant *Chlamydia pneumoniae* antigens to induce T cell proliferation and interferon- γ production is determined as follows.

Proteins are induced by IPTG and purified by Ni-NTA agarose affinity chromatography (Webb et al., *J. Immunology* 157:5034-5041, 1996). The purified polypeptides are then screened for the ability to induce T-cell proliferation in PBMC preparations. PBMCs from *C. pneumoniae* patients as well as from normal donors whose T-cells are known to proliferate in response to *Chlamydia* antigens, are cultured in medium comprising RPMI 1640 supplemented with 10% pooled human serum and 50 μ g/ml gentamicin. Purified polypeptides are added in duplicate at concentrations of 0.5 to 10 μ g/mL. After six days of culture in 96-well round-bottom plates in a volume of 200 μ l, 50 μ l of medium is removed from each well for determination of IFN- γ levels, as described below. The plates are then pulsed with 1 μ Ci/well of tritiated thymidine for a further 18 hours, harvested and tritium uptake determined using a gas scintillation counter. Fractions that result in proliferation in both replicates three fold greater than the proliferation observed in cells cultured in medium alone are considered positive.

IFN- γ was measured using an enzyme-linked immunosorbent assay (ELISA). ELISA plates are coated with a mouse monoclonal antibody directed to human IFN- γ (PharMingen, San Diego, CA) in PBS for four hours at room temperature. Wells are then blocked with PBS containing 5% (W/V) non-fat dried milk for 1 hour at room temperature. The plates are washed six times in PBS/0.2% TWEEN-20 and samples diluted 1:2 in culture medium in the ELISA plates are incubated overnight at

room temperature. The plates are again washed and a polyclonal rabbit anti-human IFN- γ serum diluted 1:3000 in PBS/10% normal goat serum is added to each well. The plates are then incubated for two hours at room temperature, washed and horseradish peroxidase-coupled anti-rabbit IgG (Sigma Chemical Co., St. Louis, MO) is added at a 1:2000 dilution in PBS/5% non-fat dried milk. After a further two hour incubation at room temperature, the plates are washed and TMB substrate added. The reaction is stopped after 20 min with 1 N sulfuric acid. Optical density is determined at 450 nm using 570 nm as a reference wavelength. Fractions that result in both replicates giving an OD two fold greater than the mean OD from cells cultured in medium alone, plus 3 standard deviations, are considered positive.

A human anti-*Chlamydia* T-cell line (TCL-8) capable of cross-reacting to *C. trachomatis* and *C. pneumonia* was used to determine whether the expressed proteins described in the example above, (i.e., CpSWIB, SEQ ID NO: 27, and SEQ ID NO: 78 having a 6X His tag, with the corresponding amino acid sequence provided in SEQ ID NO: 28, respectively, and the 15 kDa protein referred to as CpS13 SEQ ID NO: 29, and SEQ ID NO: 77, having a 6X His tag, with the corresponding amino acid sequence provided in SEQ ID NO: 30 and 91, respectively), possessed T-cell epitopes common to both *C. trachomatis* and *C. pneumonia*. Briefly, *E. coli* expressing *Chlamydial* proteins were titred on 1×10^4 monocyte-derived dendritic cells. After two hours, the dendritic cells cultures were washed and 2.5×10^4 T cells (TCL-8) added and allowed to incubate for an additional 72 hours. The amount of INF- γ in the culture supernatant was then determined by ELISA. As shown in Figs. 7A and 7B, the TCL-8 T-cell line specifically recognized the S13 ribosomal protein from both *C. trachomatis* and *C. pneumonia* as demonstrated by the antigen-specific induction of IFN- γ , whereas only the SWIB protein from *C. trachomatis* was recognized by the T-cell line. To validate these results, the T cell epitope of *C. trachomatis* SWIB was identified by epitope mapping using target cells pulsed with a series of overlapping peptides and the T-cell line TCL-8. 3H-thymidine incorporation assays demonstrated that the peptide, referred to as C.t.SWIB 52-67, of SEQ ID NO: 39 gave the strongest proliferation of the TCL-8 line. The homologous peptides corresponding to the SWIB of *C. pneumoniae* sequence (SEQ ID NO: 40), the topoisomerase-SWIB fusion of *C. pneumoniae* (SEQ ID NO: 43) and *C. trachomatis* (SEQ ID NO: 42) as well as the human SWI domain (SEQ ID NO: 41) were synthesized and tested in the above assay. The T-cell line TCL-8 only recognized the *C. trachomatis* peptide of SEQ ID NO: 39 and not the corresponding *C. pneumoniae* peptide (SEQ ID NO: 40), or the other corresponding peptides described above (SEQ ID NO: 41-43).

Chlamydia-specific T cell lines were generated from donor CP-21 with a positive serum titer against *C. pneumoniae* by stimulating donor PBMC with either *C. trachomatis* or *C. pneumoniae*-infected monocyte-derived dendritic cells, respectively. T-cells generated against *C. pneumoniae* responded to recombinant *C. pneumoniae*-SWIB but not *C. trachomatis*-SWIB, whereas the T-cell line generated against *C. trachomatis* did not respond to either *C. trachomatis*- or *C. pneumoniae*-SWIB (see Fig. 9). The *C. pneumoniae*-SWIB specific immune response of donor CP-21 confirms the *C. pneumoniae* infection and indicates the elicitation of *C. pneumoniae*-SWIB specific T-cells during *in vivo C. pneumoniae* infection.

Epitope mapping of the T-cell response to *C. pneumoniae*-SWIB has shown that Cp-SWIB-specific T-cells responded to the overlapping peptides Cp-SWIB 32-51 (SEQ ID NO: 101) and Cp-SWIB 37-56 (SEQ ID NO: 102), indicating a *C. pneumoniae*-SWIB-specific T-cell epitope Cp-SWIB 37-51 (SEQ ID NO: 100).

In additional experiments, T-cell lines were generated from donor CP1, also a *C. pneumoniae* seropositive donor, by stimulating PBMC with non-infectious elementary bodies from *C. trachomatis* and *C. pneumoniae*, respectively. In particular, proliferative responses were determined by stimulating 2.5×10^4 T-cells in the presence of 1×10^4 monocyte-derived dendritic cells and non-infectious elementary bodies derived from *C. trachomatis* and *C. pneumoniae*, or either recombinant *C. trachomatis* or *C. pneumoniae* SWIB protein. The T-cell response against SWIB resembled the data obtained with T-cell lines from CP-21 in that *C. pneumoniae*-SWIB, but not *C. trachomatis*-SWIB elicited a response by the *C. pneumoniae* T-cell line. In addition, the *C. trachomatis* T-cell line did not proliferate in response to either *C. trachomatis* or *C. pneumoniae* SWIB, though it did proliferate in response to both CT and CP elementary bodies. As described in Example 1, Clone 11-C12-91 (SEQ ID NO: 63), identified using the TCP-21 cell line, has a 269 bp insert that is part of the OMP2 gene (CT443) and shares homology with the 60 kDa cysteine rich outer membrane protein of *C. pneumoniae*, referred to as OMCB. To further define the reactive epitope(s), epitope mapping was performed using a series of overlapping peptides and the immunoassay previously described. Briefly, proliferative responses were determined by stimulating 2.5×10^4 TCP-21 T-cells in the presence of 1×10^4 monocyte-derived dendritic cells with either non-infectious elementary bodies derived from *C. trachomatis* and *C. pneumoniae*, or peptides derived from the protein sequence of *C. trachomatis* or *C. pneumoniae* OMCB protein (0.1 μ g/ml). The TCP-21 T-cells responded to epitopes CT-OMCB #167-186, CT-OMCB #171-190, CT-OMCB #171-186, and to a lesser extent, CT-OMCB #175-186 (SEQ ID NO: 249-252, respectively). Notably, the TCP-

- 21 T-cell line also gave a proliferative response to the homologous *C. pneumoniae* peptide CP-OMCB #171-186 (SEQ ID NO: 253), which was equal to or greater than the response to the *C. trachomatis* peptides. The amino acid substitutions in position two (i.e., Asp for Glu) and position four (i.e., Cys for Ser) did not alter the proliferative response of the T-cells and therefore demonstrating this epitope to be a cross-reactive epitope between *C. trachomatis* and *C. pneumoniae*.

EXAMPLE 8

IMMUNE RESPONSES OF HUMAN PBMC AND T-CELL LINES
AGAINST *CHLAMYDIA* ANTIGENS

- The examples provided herein suggest that there is a population of healthy donors among the general population that have been infected with *C. trachomatis* and generated a protective immune response controlling the *C. trachomatis* infection. These donors remained clinically asymptomatic and seronegative for *C. trachomatis*. To characterize the immune responses of normal donors against *chlamydial* antigens which had been identified by CD4 expression cloning, PBMC obtained from 12 healthy donors were tested against a panel of recombinant *chlamydial* antigens including *C. trachomatis*-, *C. pneumoniae*-SWIB and *C. trachomatis*-, *C. pneumoniae*-S13. The data are summarized in Table I below. All donors were seronegative for *C. trachomatis*, whereas 6/12 had a positive *C. pneumoniae* titer. Using a stimulation index of >4 as a positive response, 11/12 of the subjects responded to *C. trachomatis* elementary bodies and 12/12 responded to *C. pneumoniae* elementary bodies. One donor, AD104, responded to recombinant *C. pneumoniae*-S13 protein, but not to recombinant *C. trachomatis*-S13 protein, indicating a *C. pneumoniae*-specific response. Three out of 12 donors had a *C. trachomatis*-SWIB, but not a *C. pneumoniae*-SWIB specific response, confirming a *C. trachomatis* infection. *C. trachomatis* and *C. pneumoniae*-S13 elicited a response in 8/12 donors suggesting a *chlamydial* infection. These data demonstrate the ability of SWIB and S13 to elicit a T-cell response in PBMC of normal study subjects.

TABLE I

Immune response of normal study subjects against *Chlamydia*

Donor	Sex	<i>Chlamydia</i> IgG titer	CT EB	CP EB	CT Swib	CP Swib	CT S13	CP S13	CT lpdA	CT TSA
AD100	male	negative	++	+++	+	-	++	++	-	n.t.
AD104	female	negative	+++	++	-	-	-	++	-	n.t.
AD108	male	CP 1:256	++	++	+	+/-	+	+	+	n.t.
AD112	female	negative	++	++	+	-	+	-	+/-	n.t.
AD120	male	negative	-	+	-	-	-	-	-	n.t.
AD124	female	CP 1:128	++	++	-	-	-	-	-	n.t.
AD128	male	CP 1:512	+	++	-	-	++	+	++	-
AD132	female	negative	++	++	-	-	+	+	-	-
AD136	female	CP 1:128	+	++	-	-	+/-	-	-	-
AD140	male	CP 1:256	++	++	-	-	+	+	-	-
AD142	female	CP 1:512	++	++	-	-	+	+	+	-
AD146	female	negative	++	++	-	-	++	+	+	-

- CT= *Chlamydia trachomatis*; CP= *Chlamydia pneumoniae*; EB= *Chlamydia* elementary bodies; Swib= recombinant *Chlamydia* Swib protein; S13= recombinant *Chlamydia* S13 protein; lpdA= recombinant *Chlamydia* lpdA protein; TSA= recombinant *Chlamydia* TSA protein. Values represent results from standard proliferation assays. Proliferative responses were determined by stimulating 3×10^5 PBMC with 1×10^4 monocyte-derived dendritic cells pre-incubated with the respective recombinant antigens or elementary bodies (EB). Assays were harvested after 6 days with a ^3H -thymidine pulse for the last 18h.

SI: Stimulation index

+/-: SI ~ 4

+: SI > 4

++: SI 10-30

5 +++: SI > 30

In a first series of experiments, T-cell lines were generated from a healthy female individual (CT-10) with a history of genital exposure to *C. trachomatis* by stimulating T-cells with *C. trachomatis* LGV II elementary bodies as previously described. Although the study subject was exposed to *C. trachomatis*, she did not seroconvert and did not develop clinical symptoms, suggesting donor CT-10 may have developed a protective immune response against *C. trachomatis*. As shown in Fig. 10, a primary *Chlamydia*-specific T-cell line derived from donor CT-10 responded to *C. trachomatis*-SWIB, but not *C. pneumoniae*-SWIB recombinant proteins, confirming the exposure of CT-10 to *C. trachomatis*. Epitope mapping of the T-cell response to *C. trachomatis*-SWIB showed that this donor responded to the same epitope Ct-SWIB 52-67 (SEQ ID NO: 39) as T-cell line TCL-8, as shown in Fig. 11.

Additional T-cell lines were generated as described above for various *C. trachomatis* patients. A summary of the patients' clinical profile and proliferative responses to various *C. trachomatis* and *C. pneumoniae* elementary bodies and recombinant proteins are summarized in Table II.

TABLE II

Proliferative response of <i>C. trachomatis</i> patients										
Patients	Clinical manifestation	IgG titer	CT EB	CP EB	CT Swib	CP Swib	CT S13	CP S13	CT lpdA	CT TSA
CT-1	NGU	negative	+	+	-	-	++	++	++	+
CT-2	NGU	negative	++	++	-	-	+	+/-	-	-
CT-3	asymptomatic shed Eb Dx was HPV	Ct 1:512 Cp 1:1024 Cps 1:256	+	+	-	-	+	-	+	-
CT-4	asymptomatic shed Eb	Ct 1:1024	+	+	-	-	-	-	-	-
CT-5	BV	Ct 1:256 Cp 1:256	++	++	-	-	+	-	-	-
CT-6	perinial rash discharge	Cp 1:1024	+	+	-	-	-	-	-	-
CT-7	BV genital ulcer	Ct 1:512 Cp 1:1024	+	+	-	-	+	+	+	-
CT-8	Not known	Not tested	++	++	-	-	-	-	-	-
CT-9	asymptomatic	Ct 1:128 Cp 1:128	+++	++	-	-	++	+	+	-
CT-10	Itch mild vulvar	negative	++	++	-	-	-	-	-	-
CT-11	BV, abnormal pap	Ct 1: 512	+++	+++	-	-	+++	+/-	++	+
CT-12	asymptomatic	Cp 1: 512	++	++	-	-	++	+	+	-

NGU= Non-Gonococcal Urethritis; BV= Bacterial Vaginosis; CT= *Chlamydia trachomatis*; CP= *Chlamydia pneumoniae*; EB= *Chlamydia* elementary bodies; Swib= recombinant *Chlamydia* Swib protein; S13= recombinant *Chlamydia* S13 protein; lpdA= recombinant *Chlamydia* lpdA protein; TSA= recombinant *Chlamydia* TSA protein

Values represent results from standard proliferation assays. Proliferative responses were determined by stimulating 3×10^5 PBMC with 1×10^4 monocyte-

derived dendritic cells pre-incubated with the respective recombinant antigens or elementary bodies (EB). Assays were harvested after 6 days with a ³H-thymidine pulse for the last 18 hours.

5	SI: Stimulation index	
	+/-: SI ~	4
	+: SI >	4
	++: SI	10-30
	+++: SI >	30

10

Using the panel of asymptomatic (as defined above) study subjects and *C. trachomatis* patients, as summarized in Tables I and II, a comprehensive study of the immune responses of PBMC derived from the two groups was conducted. Briefly, PBMCs from *C. pneumoniae* patients as well as from normal donors are cultured in medium comprising RPMI 1640 supplemented with 10% pooled human serum and 50 μ g/ml gentamicin. Purified polypeptides, a panel of recombinant *chlamydial* antigens including *C. trachomatis*-, *C. pneumoniae*-SWIB and S13, as well as *C. trachomatis* lpdA and TSA are added in duplicate at concentrations of 0.5 to 10 μ g/mL. After six days of culture in 96-well round-bottom plates in a volume of 200 μ l, 50 μ l of medium is removed from each well for determination of IFN- γ levels, as described below. The plates are then pulsed with 1 μ Ci/well of tritiated thymidine for a further 18 hours, harvested and tritium uptake determined using a gas scintillation counter. Fractions that result in proliferation in both replicates three fold greater than the proliferation observed in cells cultured in medium alone are considered positive.

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Proliferative responses to the recombinant *Chlamydiae* antigens demonstrated that the majority of asymptomatic donors and *C. trachomatis* patients recognized the *C. trachomatis* S13 antigen (8/12) and a majority of the *C. trachomatis* patients recognized the *C. pneumoniae* S13 antigen (8/12), with 4/12 asymptomatic donors also recognizing the *C. pneumoniae* S13 antigen. Also, six out of twelve of the *C. trachomatis* patients and four out of twelve of the asymptomatic donors gave a proliferative response to the lpdA antigen of *C. trachomatis*. These results demonstrate that the *C. trachomatis* and *C. pneumoniae* S13 antigen, *C. trachomatis* Swib antigen and the *C. trachomatis* lpdA antigen are recognized by the asymptomatic donors, indicating these antigens were recognized during exposure to *Chlamydia* and an immune response elicited against them. This implies these antigens may play a role in conferring protective immunity in a human host. In addition, the *C. trachomatis* and *C. pneumoniae* S13 antigen is recognized equally well among the *C. trachomatis* patients,

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therefore indicating there may be epitopes shared between *C. trachomatis* and *C. pneumonia* in the S13 protein. Table III summarizes the results of these studies.

TABLE III

A. Antigen	NORMAL DONORS	C.T. PATIENTS
C.t.-Swib	3/12	0/12
C.p.-Swib	0/12	0/12
C.t.-S13	8/12	8/12
C.p.-S13	4/12	8/12
lpdA	4/12	6/12
TSA	0/12	2/12

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A series of studies were initiated to determine the cellular immune response to short-term T-cell lines generated from asymptomatic donors and *C. trachomatis* patients. Cellular immune responses were measured by standard proliferation assays and IFN- γ , as described in Example 7. Specifically, the majority of the antigens were in the form of single *E. coli* clones expressing Chlamydial antigens, although some recombinant proteins were also used in the assays. The single *E. coli* clones were titrated on 1×10^4 monocyte-derived dendritic cells and after two hours, the culture was washed and 2.5×10^4 T-cells were added. The assay using the recombinant proteins were performed as previously described. Proliferation was determined after four days with a standard ^3H -thymidine pulse for the last 18 hours. Induction of IFN- γ was determined from culture supernatants harvested after four days using standard ELISA assays, as described above. The results show that all the *C. trachomatis* antigens tested, except for C.T. Swib, elicited a proliferative response from one or more different T-cell lines derived from *C. trachomatis* patients. In addition, proliferative responses were elicited from both the *C. trachomatis* patients and asymptomatic donors for the following *Chlamydia* genes, CT622, groEL, pmpD, CT610 and rS13.

The 12G3-83 clone also contains sequences to CT734 and CT764 in addition to CT622, and therefore these gene sequence may also have immunoreactive epitopes. Similarly, clone 21G12-60 contains sequences to the hypothetical protein genes CT229 and CT228 in addition to CT875; and 15H2-76 also contains sequences

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from CT812 and CT088, as well as sharing homology to the *sycE* gene. Clone 11H3-61 also contains sequences sharing homology to the PGP6-D virulence protein.

TABLE IV

Clone	C. t. Antigen (putative*)	TCL from Asymp. Donors	TCL from C. t. Patients	SEQ ID NO:
1B1-66 (E. coli)	Swib	2/2	0/4	5
1B1-66 (protein)	Swib	2/2	0/4	5
12G3-83 (E. coli)	CT622*	2/2	4/4	57
22B3-53 (E. coli)	GROEL	1/2	4/4	111
22B3-53 (protein)	GROEL	1/2	4/4	111
15H2-76 (E. coli)	PMPD*	1/2	3/4	87
11H3-61 (E. coli)	rL1*	0/2	3/4	60
14H1-4 (E. coli)	TSA	0/2	3/4	56
14H1-4 (protein)	TSA	0/2	3/4	56
11G10-46 (E. coli)	CT610	1/2	1/4	62
10C10-17 (E. coli)	rS13	1/2	1/4	62
10C10-17 (protein)	RS13	1/2	1/4	62
21G12-60 (E. coli)	CT875*	0/2	2/4	110
11H4-32 (E. coli)	DNAK	0/2	2/4	59
21C7-8 (E. coli)	DNAK	0/2	2/4	115
17C10-31 (E. coli)	CT858	0/2	2/4	114

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EXAMPLE 9

PROTECTION STUDIES USING *CHLAMYDIA* ANTIGENS

Protection studies were conducted in mice to determine whether immunization with chlamydial antigens can impact on the genital tract disease resulting from chlamydial inoculation. Two models were utilized; a model of intravaginal inoculation that uses a human isolate containing a strain of *Chlamydia psittaci* (MTW447), and a model of intrauterine inoculation that involves a human isolate identified as *Chlamydia trachomatis*, serovar F (strain NI1). Both strains induce inflammation in the upper genital tract, which resemble endometritis and salpingitis caused by *Chlamydia trachomatis* in women. In the first experiment, C3H mice (4

mice per group) were immunized three times with 100 µg of pcDNA-3 expression vector containing *C. trachomatis* SWIB DNA (SEQ ID NO: 1, with the corresponding amino acid sequence provided in SEQ ID NO: 5). Inoculations were at the base of the tail for systemic immunization. Two weeks after the last immunization, animals were

5 progesterone treated and infected, either thru the vagina or by injection of the inoculum in the uterus. Two weeks after infection, the mice were sacrificed and genital tracts sectioned, stained and examined for histopathology. Inflammation level was scored (from + for very mild, to +++++ for very severe). Scores attributed to each single oviduct/ovary were summed and divided by the number of organs examined to get a

10 mean score of inflammation for the group. In the model of uterine inoculation, negative control-immunized animals receiving empty vector showed consistent inflammation with an ovary/oviduct mean inflammation score of 6.12, in contrast to 2.62 for the DNA-immunized group. In the model of vaginal inoculation and ascending infection, negative control-immunized mice had an ovary/oviduct mean inflammation score of

15 8.37, versus 5.00 for the DNA-immunized group. Also, in the later model, vaccinated mice showed no signs of tubal occlusion while negative control vaccinated groups had inflammatory cells in the lumen of the oviduct

In a second experiment, C3H mice (4 mice per group) were immunized three times with 50 µg of pcDNA-3 expression vector containing *C. trachomatis* SWIB

20 DNA (SEQ ID NO: 1, with the corresponding amino acid sequence provided in SEQ ID NO: 5) encapsulated in Poly Lactide co-Glycolide microspheres (PLG); immunizations were made intra-peritoneally. Two weeks after the last immunization, animal were progesterone treated and infected by inoculation of *C. psittaci* in the vagina. Two weeks after infection, mice were sacrificed and genital tracts sectioned, stained and

25 examined for histopathology. Inflammation level was scored as previously described. Scores attributed to each single oviduct/ovary were summed and divided by the number of examined organs to get a mean of inflammation for the group. Negative control-immunized animals receiving PLG-encapsulated empty vector showed consistent inflammation with an ovary/oviduct mean inflammation score of 7.28, versus 5.71 for the PLG-encapsulated DNA immunized group. Inflammation in the peritoneum was

30 1.75 for the vaccinated group versus 3.75 for the control.

In a third experiment, C3H mice (4 per group) were immunized three times with 10 µg of purified recombinant protein, either SWIB (SEQ ID NO: 1, with the corresponding amino acid sequence provided in SEQ ID NO: 5, or S13 (SEQ ID

35 NO: 4, with the corresponding amino acid sequence provided in SEQ ID NO: 12) mixed with Cholera Toxin (CT); the preparation was administered intranasally upon anaesthesia

in a 20 uL volume. Two weeks after the last immunization, animal were progesterone treated and infected, either by vaginal inoculation of *C. psittaci* or by injection of *C. trachomatis* serovar F in the uterus. Two weeks after infection, the mice were sacrificed and genital tracts sectioned, stained and examined for histopathology. The degree of inflammation was scored as described above. Scores attributed to each single oviduct /ovary were summed and divided by the number of examined organs to get a mean score of inflammation for the group. In the model of uterine inoculation, negative control- immunized animals receiving cholera toxin alone showed an ovary /oviduct mean inflammation score of 4.25 (only 2 mice analyzed ; 2 other died) versus 5.00 for the s13 plus cholera toxin-immunized group, and 1.00 for the SWIB plus cholera toxin. Untreated infected animals had an ovary /oviduct mean inflammation score of 7. In the model of vaginal inoculation and ascending infection, negative control-immunized mice had an ovary /oviduct mean inflammation score of 7.37 versus 6.75 for the s13 plus cholera toxin-immunized group and 5.37 for the SWIB plus cholera toxin-immunized group. Untreated infected animals had an ovary /oviduct mean inflammation score of 8.

The three experiments described above suggest that SWIB-specific protection is obtainable. This protective effect is more marked in the model of homologous infection but is still present when in a heterologous challenge infection with *C. psittaci*.

EXAMPLE 10

PMP/RA12 FUSION PROTEINS

Various Pmp/Ra12 fusion constructs were generated by first synthesizing PCR fragments of a Pmp gene using primers containing a Not I restriction site. Each PCR fragment was then ligated into the NotI restriction site of pCRX1. The pCRX1 vector contains the 6HisRa12 portion of the fusion. The Ra12 portion of the fusion construct encodes a polypeptide corresponding to amino acid residues 192-323 of *Mycobacterium tuberculosis* MTB32A, as described in U.S. Patent Application 60/158,585, the disclosure of which is incorporated herein by reference. The correct orientation of each insert was determined by its restriction enzyme pattern and its sequence was verified. Multiple fusion constructs were made for PmpA, PmpB, PmpC, PmpF and PmpH, as described further below:

PMPA FUSION PROTEINS

PmpA is 107 kD protein containing 982 aa and was cloned from serovar E. The PmpA protein was divided into 2 overlapping fragments, the PmpA(N-terminal) and (C-terminal) portions.

PmpA(N-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCATGTTTATAACAAAGGAACTTATG (SEQ ID NO:306)

GAGAGCGGCCGCTTACTTAGGTGAGAAGAAGGAGTTTC (SEQ ID NO:307)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 308, encoding a 66 kD protein (619aa) expressing the segment 1-473 aa of PmpA. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 309.

PmpA(C-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCCATTCTATTCATTCTTTGATCCTG (SEQ ID NO:310)

GAGAGCGGCCGCTTAGAAGCCAACATAGCCTCC (SEQ ID NO:311)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 312, encoding a 74 kD protein (691aa) expressing the segment 438-982 aa of PmpA. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 313.

PMPF FUSION PROTEINS

PmpF is 112 kD protein containing 1034 aa and was cloned from the serovar E. PmpF protein was divided into 2 overlapping fragments, the PmpF(N-term) and (C-term) portions.

PmpF(N-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCATGATTAAGAACTTCTCTATCC (SEQ ID NO:314)

GAGAGCGGCCGCTTATAATTCTGCATCATCTTCTATGGC (SEQ ID NO:315)

respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 316, encoding a 69 kD protein (646aa) expressing the segment 1-499 aa of PmpF. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 317.

PmpF(C-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGACATACGAACCTCTGATGGG (SEQ ID NO:318)

5 GAGAGCGGCCGCTTAAAAGACCAGAGCTCCTCC (SEQ ID NO:319)

respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 320, encoding a 77 kD protein (715aa) expressing the segment 466-1034aa of PmpF. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 321.

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PMPH FUSION PROTEINS

PmpH is 108 kD protein containing 1016 aa and was cloned from the serovar E. PmpH protein was divided into 2 overlapping fragments, the PmpH(N-term) and (C-term) portions.

PmpH(N-term) was amplified by the sense and antisense primers:

15 GAGAGCGGCCGCTCATGCCCTTTTCTTTGAGATCTAC (SEQ ID NO:322)

GAGAGCGGCCGCTTACACAGATCCATTACCGGACTG (SEQ ID NO:323)

20 respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 324, encoding a 64 kD protein (631aa) expressing the segment 1-484 aa of PmpH. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 325.

PmpH(C-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGATCCTGTAGTACAAAATAATTCAGC (SEQ ID NO:326)

25 GAGAGCGGCCGCTTAAAAGATTCTATTCAAGCC (SEQ ID NO:327)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 328, encoding a 77 kD protein (715aa) expressing the segment 449-1016aa of PmpH. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 329.

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PMPB FUSION PROTEINS

PmpB is 183 kD protein containing 1750 aa and was cloned from the serovar E. PmpB protein was divided into 4 overlapping fragments, PmpB(1), (2), (3) and (4).

35 PmpB(1) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCATGAAATGGCTGTGCTCAGCTACTGCG (SEQ ID NO:330)

GAGAGCGGCCGCTTACTTAATGCGAATTCTTCAAG (SEQ ID NO:331)

- 5 respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 332, and encodes a 53 kD protein (518aa) expressing the segment 1-372 aa of PmpB. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 333.

PmpB(2) was amplified by the sense and antisense primers:

10 GAGAGCGGCCGCTCGGTGACCTCTCAATCAATCTTC (SEQ ID NO:334)

GAGAGCGGCCGCTTAGTTCTCTGTTACAGATAAGGAGAC (SEQ ID NO:335)

- respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 336 and encodes a 60 kD protein (585aa) expressing the segment 330-767 aa of PmpB. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 337.

PmpB(3) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGACCAACTGAATATCTCTGAGAAC (SEQ ID NO:338)

20 GAGCGGCCGCTTAAGAGACTACGTGGAGTTCTG (SEQ ID NO:339)

- respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 340 encodes a 67 kD protein (654aa) expressing the segment 732-1236 aa of PmpB. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 341

PmpB(4) was amplified by the sense and antisense primers:

25 GAGAGCGGCCGCTCGGAACATTGTGTTCTCTTCTG (SEQ ID NO:342)

GAGAGCGGCCGCTTAGAAGATCATGCGAGACCCGC (SEQ ID NO:343)

- 30 respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 344 encodes a 76 kD protein (700aa) expressing the segment 1160-1750 of PmpB. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 345.

PMPC FUSION PROTEINS

PmpC is 187 kD protein containing 1774 aa and was cloned from the serovar E/L2. PmpC protein was divided into 3 overlapping fragments, PmpC(1), (2) and (3).

PmpC(1) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCATGAAATTTATGTCAGCTACTGC (SEQ ID NO:346)

GAGAGCGGCCGCTTACCCTGTAATTCCAGTGATGGTC (SEQ ID NO:347)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 348 and encodes a 51 kD protein (487aa) expressing the segment 1-340 aa of PmpC. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 349.

PmpC(2) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGATACACAAGTATCAGAATCACC (SEQ ID NO:350)

GAGAGCGGCCGCTTAAGAGGACGATGAGACACTCTCG (SEQ ID NO:351)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 352 and encodes a 60 kD protein (583aa) expressing the segment 305-741 aa of PmpC. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 353.

PmpC(3) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGATCAATCTAACGAAAACACAGACG (SEQ ID NO:354)

GAGAGCGGCCGCTTAGACCAAAGTCCATCAGCAAC (SEQ ID NO:355)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 356 and encodes a 70 kD protein (683aa) expressing the segment 714-1250 aa of PmpC. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 357.

Although the present invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, changes and modifications can be carried out without departing from the scope of the invention which is intended to be limited only by the scope of the appended claims.

CLAIMS

1. An isolated polypeptide comprising an immunogenic portion of a *Chlamydia* antigen, wherein said antigen comprises an amino acid sequence encoded by a polynucleotide sequence selected from the group consisting of: (a) sequences recited in SEQ ID NO: 169-174, 181-188, 263, 265 and 267-290 ; (b) sequences complementary to a sequence of (a); and (c) polynucleotide sequences that hybridize to a sequence of (a) or (b) under moderately stringent conditions.
2. The polypeptide of claim 1 wherein the polypeptide comprises a sequence selected from the group consisting of SEQ ID NO: 175-180, 189-196, 264 and 266.
3. An isolated polynucleotide molecule comprising a nucleotide sequence encoding a polypeptide according to any one of claims 1 and 2.
4. A recombinant expression vector comprising a polynucleotide molecule according to claim 3.
5. A host cell transformed with an expression vector according to claim 4.
6. The host cell of claim 5 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cells.
7. A fusion protein comprising a polypeptide according to any one of claims 1 and 2.
8. A fusion protein according to claim 7, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with a polynucleotide encoding the fusion protein.
9. A fusion protein according to claim 7, wherein the fusion protein comprises a T helper epitope that is not present within the polypeptide of claim 1.
10. A fusion protein according to claim 7, wherein the fusion protein comprises an affinity tag.

11. An isolated polynucleotide encoding a fusion protein according to claim 7.
12. An isolated monoclonal antibody, or antigen-binding fragment thereof, that specifically binds to a Chlamydia protein that comprises an amino acid sequence that is encoded by a polynucleotide sequence according to claim 1, or a complement of any of the foregoing polynucleotide sequences.
13. A pharmaceutical composition comprising a polypeptide according to claim 1, and a physiologically acceptable carrier.
14. A pharmaceutical composition comprising a polynucleotide molecule according to claim 3 and a physiologically acceptable carrier.
15. A pharmaceutical composition comprising a polypeptide and a physiologically acceptable carrier, wherein the polypeptide is encoded by polynucleotide molecule selected from the group consisting of: (a) sequences recited in SEQ ID NO: 169-174, 181-188, 263, 265 and 267-291; (b) sequences complementary to a sequence of (a); and (c) sequences that hybridize to a sequence of (a) or (b) under moderately stringent conditions.
16. A pharmaceutical composition comprising a polynucleotide molecule and a physiologically acceptable carrier, wherein the polynucleotide molecule comprises a sequence selected from the group consisting of: (a) sequences recited in SEQ ID NO: 169-174, 181-188, 263, 265 and 267-291; (b) sequences complementary to a sequence of (a); and (c) sequences that hybridize to a sequence of (a) or (b) under moderately stringent conditions.
17. A pharmaceutical composition comprising a physiologically acceptable carrier and at least one component selected from the group consisting of:
 - (a) a fusion protein according to claim 7;
 - (b) a polynucleotide according to claim 11; and
 - (c) an antibody according to claim 12.
18. A vaccine comprising a polypeptide according to claim 1, and an immunostimulant.

19. A vaccine comprising a polynucleotide molecule according to claim 3 and an immunostimulant.
20. A vaccine comprising a polypeptide and an immunostimulant, wherein the polypeptide is encoded by a sequence selected from the group consisting of: (a) sequences recited in SEQ ID NO: 169-174, 181-188, 263, 265 and 267-291; (b) sequences complementary to a sequence of (a); and (c) sequences that hybridize to a sequence of (a) or (b) under moderately stringent conditions.
21. A vaccine comprising a DNA molecule and an immunostimulant, wherein the DNA molecule comprises a sequence selected from the group consisting of: (a) sequences recited in SEQ ID NO: 169-174, 181-188, 263, 265 and 267-291; (b) sequences complementary to a sequence of (a); and (c) sequences that hybridize to a sequence of (a) or (b) under moderately stringent conditions.
22. A vaccine comprising an immunostimulant and at least one component selected from the group consisting of:
- (a) a fusion protein according to claim 7;
 - (b) a polynucleotide according to claim 11; and
 - (c) an antibody according to claim 12.
23. The vaccine of any one of claims 18-22 wherein the immunostimulant is an adjuvant.
24. A method for inducing protective immunity in a patient, comprising administering to a patient a pharmaceutical composition according to any one of claims 13-17.
25. A method for inducing protective immunity in a patient, comprising administering to a patient a vaccine according to any one of claims 18-22.
26. An isolated polyclonal antibody, or antigen-binding fragment thereof, that specifically binds to a Chlamydia protein that comprises an amino acid sequence that is encoded by a polynucleotide sequence according to claim 1, or a complement of any of the foregoing polynucleotide sequences.

27. A method for detecting *Chlamydia* infection in a patient, comprising:
- (a) obtaining a biological sample from the patient;
 - (b) contacting the sample with a polypeptide comprising an immunogenic portion of a *Chlamydia* antigen, wherein said antigen comprises an amino acid sequence encoded by a polynucleotide sequence selected from the group consisting of: (i) a sequence recited in SEQ ID NO: 169-174, 181-188, 263, 265 and 267-291. (ii) sequences complementary to a sequence of (i), and (c) polynucleotide sequences that hybridize to a sequence of (i) or (ii) under moderately stringent conditions; and
 - (c) detecting the presence of antibodies that bind to the polypeptide.
28. A method for detecting *Chlamydia* infection in a patient, comprising:
- (a) obtaining a biological sample from the patient;
 - (b) contacting the sample with a fusion protein comprising a polypeptide, the polypeptide comprising an immunogenic portion of a *Chlamydia* antigen, wherein said antigen comprises an amino acid sequence encoded by a polynucleotide sequence selected from the group consisting of (i) a sequence recited in SEQ ID NO: 169-174, 181-188, 263, 265 and 267-291 (ii) sequences complementary to a sequence of (i), and (c) polynucleotide sequences that hybridize to a sequence of (i) or (ii) under moderately stringent conditions; and
 - (c) detecting the presence of antibodies that bind to the fusion protein.
29. The method of any one of claims 27 and 28 wherein the biological sample is selected from the group consisting of whole blood, serum, plasma, saliva, cerebrospinal fluid and urine.
30. A method for detecting *Chlamydia* infection in a biological sample, comprising:
- (a) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotide primers is specific for a polynucleotide molecule comprising a sequence of SEQ ID NO: 169-174, 181-188, 263, 265 and 267-291; and
 - (b) detecting in the sample a polynucleotide sequence that amplifies in the presence of the oligonucleotide primers, thereby detecting *Chlamydia* infection.

31. The method of claim 30, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a polynucleotide sequence of SEQ ID NO: 169-174, 181-188, 263, 265 and 267-291.

32. A method for detecting *Chlamydia* infection in a biological sample, comprising:

(a) contacting the sample with one or more oligonucleotide probes specific for a polynucleotide molecule comprising a sequence of SEQ ID NO: 169-174, 181-188, 263, 265 and 267-291; and

(b) detecting in the sample a polynucleotide sequence that hybridizes to the oligonucleotide probe, thereby detecting *Chlamydia* infection.

33. The method of claim 32 wherein the probe comprises at least about 15 contiguous nucleotides of a polynucleotide sequence of SEQ ID NO: 169-174, 181-188, 263, 265 and 267-291.

34. A method for detecting *Chlamydia* infection in a biological sample, comprising:

(a) contacting the biological sample with a binding agent which is capable of binding to a polypeptide comprising an immunogenic portion of a *Chlamydia* antigen, wherein said antigen comprises an amino acid sequence encoded by a polynucleotide sequence selected from the group consisting of: (i) a sequence recited in SEQ ID NO: 169-174, 181-188, 263, 265 and 267-291, (ii) sequences complementary to a sequence of (i), and (c) polynucleotide sequences that hybridize to a sequence of (i) or (ii) under moderately stringent conditions; and

(b) detecting in the sample a polypeptide that binds to the binding agent, thereby detecting *Chlamydia* infection in the biological sample.

35. A method of detecting *Chlamydia* infection in a biological sample, comprising:

(a) contacting the biological sample with a binding agent which is capable of binding to a fusion protein comprising a polypeptide, the polypeptide comprising an immunogenic portion of a *Chlamydia* antigen, wherein said antigen comprises an amino acid sequence encoded by a polynucleotide sequence selected from the group consisting of: (i) a sequence recited in SEQ ID NO: 169-174, 181-188, 263, 265 and 267-291, (ii) sequences

complementary to a sequence of (i), and (c) polynucleotide sequences that hybridize to a sequence of (i) or (ii) under moderately stringent conditions; and

(b) detecting in the sample a polypeptide that binds to the binding agent, thereby detecting *Chlamydia* infection in the biological sample.

36. The method of any one of claims 34 and 35 wherein the binding agent is a monoclonal antibody.

37. The method of any one of claims 34 and 35 wherein the binding agent is a polyclonal antibody.

38. The method of any one of claims 34 and 35 wherein the biological sample is selected from the group consisting of whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid and urine.

39. A diagnostic kit comprising:

(a) a polypeptide comprising an immunogenic portion of a *Chlamydia* antigen, wherein said antigen comprises an amino acid sequence encoded by a polynucleotide sequence selected from the group consisting of: (i) a sequence recited in SEQ ID NO: 169-174, 181-188, 263, 265 and 267-291, (ii) sequences complementary to a sequence of (i), and (c) polynucleotide sequences that hybridize to a sequence of (i) or (ii) under moderately stringent conditions; and

(b) a detection reagent.

40. A diagnostic kit comprising:

(a) a fusion protein comprising a polypeptide, the polypeptide comprising an immunogenic portion of a *Chlamydia* antigen, wherein said antigen comprises an amino acid sequence encoded by a polynucleotide sequence selected from the group consisting of: (i) a sequence recited in SEQ ID NO: 169-174, 181-188, 263, 265 and 267-291 (ii) sequences complementary to a sequence of (i), and (c) polynucleotide sequences that hybridize to a sequence of (i) or (ii) under moderately stringent conditions; and

(b) a detection reagent.

41. The kit of claims 39 or 40 wherein the polypeptide is immobilized on a solid support.

42. The kit of claims 39 or 40 wherein the detection reagent comprises a reporter group conjugated to a binding agent.

43. The kit of claim 42 wherein the binding agent is selected from the group consisting of anti-immunoglobulins, Protein G, Protein A and lectins.

44. The kit of claim 42 wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

45. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the oligonucleotide primers being specific for a polynucleotide molecule comprising a polynucleotide sequence of SEQ ID NO: 169-174, 181-188, 263, 265 and 267-291.

46. A diagnostic kit according to claim 43, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a sequence of SEQ ID NO: 169-174, 181-188, 263, 265 and 267-291.

47. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe being specific for a polynucleotide molecule comprising a sequence of SEQ ID NO: 169-174, 181-188, 263, 265 and 267-291.

48. A kit according to claim 47, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a polynucleotide sequence of SEQ ID NO: 169-174, 181-188, 263, 265 and 267-291.

49. A diagnostic kit comprising:

(a) at least one antibody, or antigen-binding fragment thereof, according to claim 22; and

(b) a detection reagent.

50. A method for treating *Chlamydia* infection in a patient, comprising the steps of:

(a) obtaining peripheral blood cells from the patient;

(b) incubating the cells in the presence of at least one polypeptide, the polypeptide comprising an immunogenic portion of a *Chlamydia* antigen, wherein said antigen comprises an amino acid sequence encoded by a polynucleotide sequence selected from the group consisting of: (i) a sequence recited in SEQ ID NO: 169-174, 181-188, 263, 265 and 267-291 (ii) sequences complementary to a sequence of (i), and (c) polynucleotide sequences that hybridize to a sequence of (i) or (ii) under moderately stringent conditions, such that T cells proliferate; and

(c) administering to the patient the proliferated T cells.

51. A method for treating *Chlamydia* infection in a patient, comprising the steps of:

(a) obtaining peripheral blood cells from the patient;

(b) incubating the cells in the presence of at least one polynucleotide, comprises a polynucleotide sequence selected from the group consisting of: (i) a sequence recited in SEQ ID NO: 169-174, 181-188, 263, 265 and 267-291 (ii) sequences complementary to a sequence of (i), and (c) polynucleotide sequences that hybridize to a sequence of (i) or (ii) under moderately stringent conditions, such that T cells proliferate; and

(c) administering to the patient the proliferated T cells.

52. The method of any one of claims 50 and 51 wherein the step of incubating the T cells is repeated one or more times.

53. The method of any one of claims 50 and 51 wherein step (a) further comprises separating T cells from the peripheral blood cells, and the cells incubated in step (b) are the T cells.

54. The method of any one of claims 50 and 51 wherein step (a) further comprises separating CD4+ cells or CD8+ T cells from the peripheral blood cells, and the cells proliferated in step (b) are CD4+ or CD8+ T cells.

55. The method of any one of claims 50 and 51 wherein step (a) further comprises separating gamma/delta T lymphocytes from the peripheral blood cells, and the cells proliferated in step (b) are gamma/delta T lymphocytes.

56. The method of any one of claims 50 and 51 wherein step (b) further comprises cloning one or more T cells that proliferated in the presence of the polypeptide.

57. A pharmaceutical composition for the treatment of *Chlamydia* infection in a patient, comprising T cells proliferated in the presence of a polypeptide of claim 1, in combination with a physiologically acceptable carrier.

58. A pharmaceutical composition for the treatment of *Chlamydia* infection in a patient, comprising T cells proliferated in the presence of a polynucleotide of claim 3, in combination with a physiologically acceptable carrier.

59. A method for treating *Chlamydia* infection in a patient, comprising the steps of:

- (a) incubating antigen presenting cells in the presence of at least one polypeptide of claim 1;
- (b) administering to the patient the incubated antigen presenting cells.

60. A method for treating *Chlamydia* infection in a patient, comprising the steps of:

- (a) introducing at least one polynucleotide of claim 3 into antigen presenting cells;
- (b) administering to the patient the antigen presenting cells.

61. The method of claims 59 or 60 wherein the antigen presenting cells are selected from the group consisting of dendritic cells, macrophage cells, B cells fibroblast cells, monocyte cells, and stem cells.

62. A pharmaceutical composition for the treatment of *Chlamydia* infection in a patient, comprising antigen presenting cells incubated in the presence of a polypeptide of claim 1, in combination with a physiologically acceptable carrier.

63. A pharmaceutical composition for the treatment of *Chlamydia* infection in a patient, comprising antigen presenting cells incubated in the presence of a polynucleotide of claim 3, in combination with a physiologically acceptable carrier.

64. A polypeptide comprising an immunogenic portion of a *Chlamydia* antigen, wherein said immunogenic portion comprises a sequence of SEQ ID NO: 246, 247 and 254-256.

65. An immunogenic epitope of a *Chlamydia* antigen, comprising a sequence of SEQ ID NO: 246, 247 or 254-256.

66. An isolated polypeptide comprising a sequence recited in any one of SEQ ID NO: 224-262, 246, 247, 254-256, 292 and 294-305.

67. A recombinant fusion polypeptide comprising a an amino acid sequence of a Ra12 polypeptide and an amino acid sequence of a Chlamydial polypeptide.

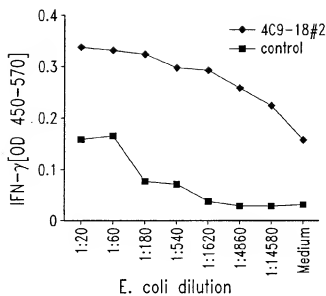
68. The recombinant polypeptide of claims 67, wherein the Chlamydial polypeptide is a Pmp polypeptide.

69. The recombinant polypeptide of claims 67, wherein the Chlamydial polypeptide is a PmpA, PmpF, PmpH, PmpB, or PmpC.

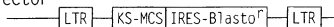
70. The recombinant polypeptide of claims 67, wherein the amino acid sequence of the fusion polypeptide is a sequence selected from the group consisting of SEQ ID NOs: 309, 313, 317, 321, 325, 329, 333, 337, 341, 345, 349, 353 and 357.

71. A recombinant DNA molecule encoding a fusion polypeptide according to claim 67.

1/10

*Fig. 1*

2/10

Retroviral vector
pBIB-KS

Kozak-Start

GA TCT	GCC GCC ACC	ATG	GAA TTC GAT ATC GGA TCC CTG CAG
A	CGG CGG TGG	TAC	CTT AAG CTA TAG CCT AGG GAC GTC
(Bg1II)		EcoRI	BamHI PstI

ReadingFrame 1
KS1+

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TTC GAA	CTC GAG CTC GCG CGG GCG	ATT	AAT CGA CTC AGC T
HinDIII	XhoI	NotI	Stop Stop Stop (SalI)

Kozak-Start

GA TCT	GCC GCC ACC	ATG	GGA ATT CGA TAT CGG ATC CCT GCA G
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(Bg1II)		EcoRI	BamHI PstI

ReadingFrame 1
KS2+

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Kozak-Start

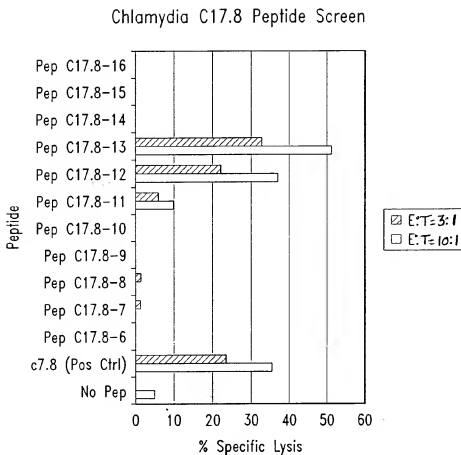
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ReadingFrame 3
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Fig. 2

3/10

*Fig. 3*

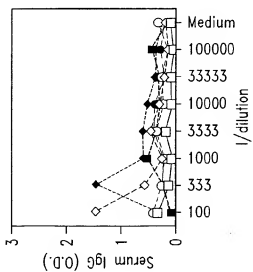


Fig. 4A

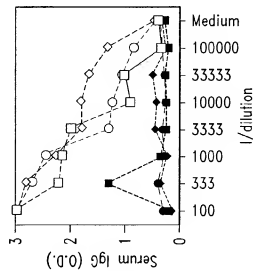


Fig. 4B

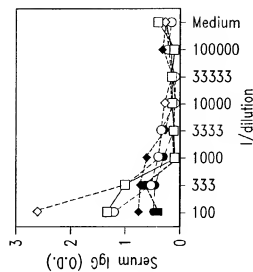
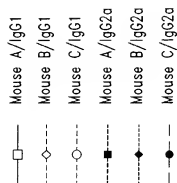


Fig. 4C



5/10

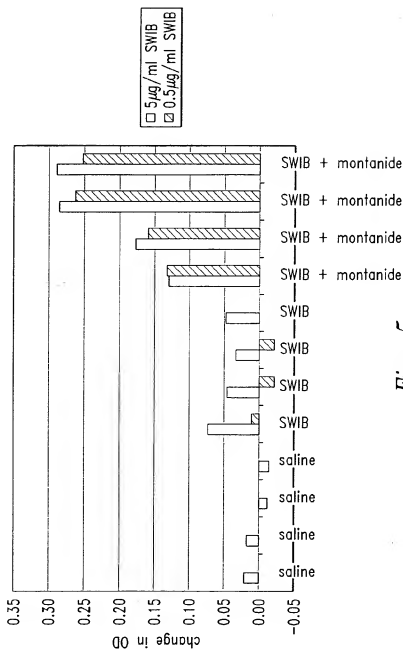


Fig. 5

6/10

CP SWIB Nde (5' primer)

5' GATATACATATGCATCACCATCACCATCACATGAGTCAAAAAATAAAAACTCT

CP SWIB EcoRI (3' primer)

5' CTCGAGGAATTCTTATTTACAATATGTTTGA

CP S13 Nde (5' primer)

5' GATATACATATGCATCACCATCACCATCACATGCCACGCATCATTGGAATGAT

CP S13 EcoRI (3' primer)

5' CTCGAGGAATTCTTATTTCTTACCTGC

Fig. 6

7/10

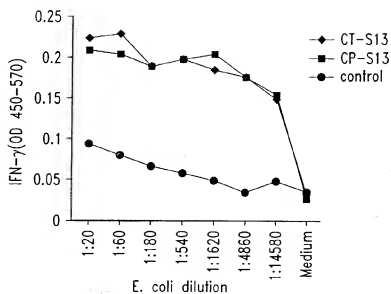


Fig. 7A

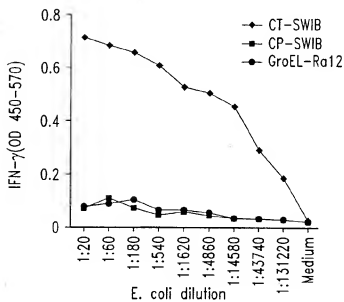
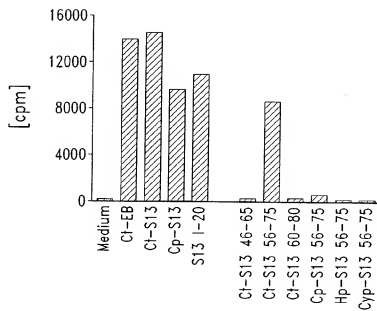
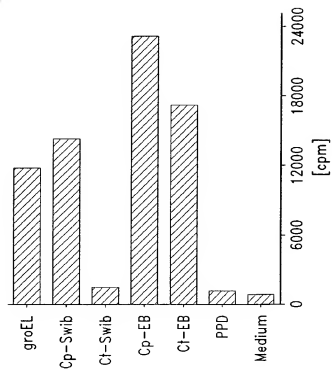
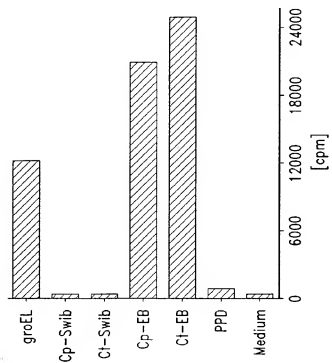


Fig. 7B

8/10

*Fig. 8*

9/10

*Fig. 9B**Fig. 9A*

10/10

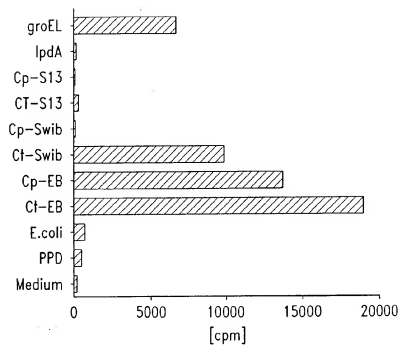


Fig. 10

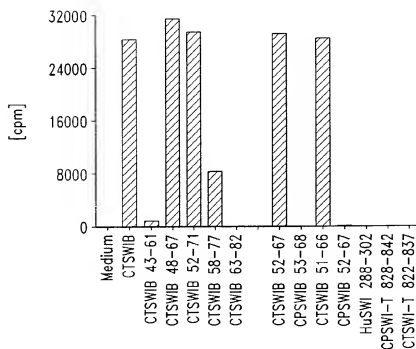


Fig. 11

SEQUENCE LISTING

<110> Corixa Corporation
 Probst, Peter
 Bhatia, Ajay
 Skeiky, Yasir A. W.
 Fling, Steven P.
 Scholler, John

<120> COMPOSITIONS AND METHODS FOR TREATMENT AND
 DIAGNOSIS OF CHLAMYDIAL INFECTION

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35 40 45
Pro Thr Asn Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys Val
50 55 60
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<212> PRT
<213> Chlamydia trachomatis

<400> 6
Ile Val Gly Ala Gly Pro Met Pro Arg Thr Glu Ile Ile Lys Lys Met
1 5 10 15
Trp Asp Tyr Ile Lys Glu Asn Ser Leu Gln Asp Pro Thr Asn Lys Arg
20 25 30
Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys Val Phe Gly Thr Glu Lys
35 40 45
Pro Ile Asp Met Phe Gln Met Thr Lys Met Val Ser Gln
50 55 60

<210> 7
<211> 36
<212> PRT
<213> Chlamydia trachomatis

<400> 7
 Ala Ala Thr Ser Cys Glu Leu Ala Asn Gln His Gly His Leu Gln Phe
 1 5 10 15
 Pro Leu Leu Thr Arg Ser Leu Glu Leu Met Leu Leu Pro Ser Gln Ser
 20 25 30
 Gln Ser His Arg
 35

<210> 8
 <211> 18
 <212> PRT
 <213> Chlamydia trachomatis

<400> 8
 Leu Arg His His Ala Ser Leu Gln Thr Asn Met Asp Ile Ser Asn Phe
 1 5 10 15
 Pro Phe

<210> 9
 <211> 5
 <212> PRT
 <213> Chlamydia trachomatis

<400> 9
 Leu Ala Leu Trp Asn
 1 5

<210> 10
 <211> 11
 <212> PRT
 <213> Chlamydia trachomatis

<400> 10
 Cys Cys Tyr Arg Val Asn His Asn His Ile Asp
 1 5 10

<210> 11
 <211> 36
 <212> PRT
 <213> Chlamydia trachomatis

<400> 11
 Val Asp Val Ile Val Ile Asp Ser Val Ala Ala Leu Val Pro Lys Ser
 1 5 10 15
 Glu Leu Glu Gly Glu Ile Gly Asp Val His Val Gly Leu Gln Ala Arg
 20 25 30
 Met Met Ser Gln
 35

<210> 12
 <211> 122
 <212> PRT
 <213> Chlamydia trachomatis

<400> 12
 Met Pro Arg Ile Ile Gly Ile Asp Ile Pro Ala Lys Lys Lys Leu Lys

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1           5           10           15
Ile Ser Leu Thr Tyr Ile Tyr Gly Ile Gly Pro Ala Leu Ser Lys Glu
      20      25      30
Ile Ile Ala Arg Leu Gln Leu Asn Pro Glu Ala Arg Ala Ala Glu Leu
      35      40      45
Thr Glu Glu Glu Val Gly Arg Leu Asn Ala Leu Gln Ser Asp Tyr
      50      55      60
Val Val Glu Gly Asp Leu Arg Arg Arg Val Gln Ser Asp Ile Lys Arg
      65      70      75      80
Leu Ile Thr Ile His Ala Tyr Arg Gly Gln Arg His Arg Leu Ser Leu
      85      90      95
Pro Val Arg Gly Gln Arg Thr Lys Thr Asn Ser Arg Thr Arg Lys Gly
      100      105      110
Lys Arg Lys Thr Ile Ala Gly Lys Lys Lys
      115      120

```

```

<210> 13
<211> 20
<212> PRT
<213> Chlamydia trachomatis

```

```

<400> 13
Asp Pro Thr Asn Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys
1           5           10           15
Val Phe Gly Thr
      20

```

```

<210> 14
<211> 20
<212> PRT
<213> Chlamydia trachomatis

```

```

<400> 14
Asp Asp Lys Leu Ala Lys Val Phe Gly Thr Glu Lys Pro Ile Asp Met
1           5           10           15
Phe Gln Met Thr
      20

```

```

<210> 15
<211> 161
<212> DNA
<213> Chlamydia trachomatis

```

```

<400> 15
atctttgtgt gtctcataag cgcagagcgg ctgcggctgt ctgtagcttc atcggaggaa      60
ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac aaaatgctgg      120
cgcaaccgtt tctttcttcc caaactaaag caaatatggg a                          161

```

```

<210> 16
<211> 897
<212> DNA
<213> Chlamydia trachomatis

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<400> 16
atggcttctta tatgcggagc tttagggctc ggtacaggga atgctctaaa agcttttttt      60
acacagccca acaataaaaat gccaaaggga gtaaataaga cgaagggaat ggataagact      120
attaaggttg ccaagctcgc tgcgaattg accgcaataa ttttggaaca agctgagggc      180
gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggaatgcgaga      240

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```

actgtgtgtcg ctttagggaa tgcctttaac ggagcgttgc caggaacagt tcaaaagtgcg 300
caaagcttct tctctcacat gaaagctgct agtcagaaaa cgcaagaagg ggaatgagggg 360
ctcacagcag atctttgtgt gtctcataag cgcagagcgg ctgcggctgt ctgtagcatc 420
atcgaggagaa ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac 480
aaaatgctgg caaaaccgtt tcttctctcc caaactaaag caaatatggg atcttctgtt 540
agctatatta tggcggctaa ccatgcagcg tctgtggtgg gtgcgtggact cgctatcaagt 600
gcggaaagag cagattgcga agccgcgtgc gctcgtattg cgagagaaga gtctgtactc 660
gaagtgcggg gagaggaaaa tgcttgcgag aagaaagtgc ctggagagaa agccaagacg 720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttgga atgcgttgcc 780
gacgttttca aattggtgcc gctgcctatt acaatgggta ttcgtcgat tgtggctgct 840
ggatgtacgt tcactttcgc aattattgga ttgtgcactt tctgcgccag agcataa 897

```

<210> 17

<211> 298

<212> PRT

<213> Chlamydia trachomatis

<400> 17

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Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
1 5 10 15
Lys Ala Phe Phe Thr Gln Pro Asn Asn Lys Met Ala Arg Val Val Asn
20 25 30
Lys Thr Lys Gly Met Asp Lys Thr Ile Lys Val Ala Lys Ser Ala Ala
35 40 45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
50 55 60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
65 70 75 80
Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
85 90 95
Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
100 105 110
Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
115 120 125
His Lys Arg Arg Ala Ala Ala Val Cys Ser Ile Ile Gly Gly Ile
130 135 140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
145 150 155 160
Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
165 170 175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
180 185 190
Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
195 200 205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Pro Gly
210 215 220
Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr
225 230 235 240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
245 250 255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
260 265 270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
275 280 285
Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
290 295

```

<210> 18

<211> 18
 <212> PRT
 <213> Chlamydia trachomatis

<400> 18
 Arg Ala Ala Ala Ala Ala Val Cys Ser Phe Ile Gly Gly Ile Thr
 1 5 10 15
 Tyr Leu

<210> 19
 <211> 18
 <212> PRT
 <213> Chlamydia trachomatis

<400> 19
 Cys Ser Phe Ile Gly Gly Ile Thr Tyr Leu Ala Thr Phe Gly Ala Ile
 1 5 10 15
 Arg Pro

<210> 20
 <211> 216
 <212> PRT
 <213> Chlamydia trachomatis

<400> 20
 Met Arg Gly Ser Gln Gln Ile Phe Val Cys Leu Ile Ser Ala Glu Arg
 1 5 10 15
 Leu Arg Leu Ser Val Ala Ser Ser Glu Glu Leu Pro Thr Ser Arg His
 20 25 30
 Ser Glu Leu Ser Val Arg Phe Cys Leu Ser Thr Lys Cys Trp Gln Asn
 35 40 45
 Arg Phe Phe Leu Pro Lys Leu Lys Gln Ile Trp Asp Leu Leu Ala
 50 55 60
 Ile Leu Trp Arg Leu Thr Met Gln Arg Leu Trp Trp Val Leu Asp Ser
 65 70 75 80
 Leu Ser Val Arg Lys Glu Gln Ile Ala Lys Pro Ala Ala Leu Val Leu
 85 90 95
 Arg Glu Lys Ser Arg Tyr Ser Lys Cys Arg Glu Arg Lys Met Leu Ala
 100 105 110
 Arg Arg Lys Ser Leu Glu Arg Lys Pro Arg Arg Ser Arg Ala Ser Ser
 115 120 125
 Met His Ser Ser Leu Cys Ser Arg Ser Phe Trp Asn Ala Leu Pro Thr
 130 135 140
 Phe Ser Asn Trp Cys Arg Cys Leu Leu Gln Trp Val Phe Val Arg Leu
 145 150 155 160
 Trp Leu Leu Asp Val Arg Ser Leu Leu Gln Leu Leu Asp Cys Ala Leu
 165 170 175
 Ser Ala Pro Glu His Lys Gly Phe Phe Lys Phe Leu Lys Lys Lys Ala
 180 185 190
 Val Ser Lys Lys Lys Gln Pro Phe Leu Ser Thr Lys Cys Leu Ala Phe
 195 200 205
 Leu Ile Val Lys Ile Val Phe Leu
 210 215

<210> 21
 <211> 1256

<212> DNA

<213> Chlamydia trachomatis

<400> 21

ctcgtgcccgc	cacgagcaaa	gaaatccctc	aaaaaatggc	cattattggc	gggtggtgga	60
tcgggttcgga	attcgtcttc	ttattccata	cgttaggctc	cgaagtttct	gtgatcgaag	120
caagctctca	aatccttgct	ttgaataatc	cagatatttc	aaaaaccatg	ttcgataaat	180
tcacccgaca	aggactccgt	ttcgtactag	aagcctctgt	atcaaatatt	gaggatatag	240
gagatcgcg	tcggttaact	atcaatggga	atgtcgaaga	atacagattac	gttcctcgat	300
ctataggagc	cogtttgaat	acagaaaata	ttggcttgga	taaagctggg	gttattttgt	360
atgaacgcgg	agtcacccct	accgatgcc	caatgcgcac	aaacgtacct	aacatttatg	420
ctattggaga	tatcacagga	aaatggcaac	ttgcccatgt	agcttctcat	caaggaatca	480
ttgcagcagc	gaatatagg	ggccataaag	aggaataatc	ttactctgct	gtccctctgt	540
tgatctttac	cttccctgaa	gtcgtctcag	taggcctctc	cccaacagca	gctcaacaac	600
atctctctct	tcgcttactt	tttctgaaaa	atttgatata	gaagaagaat	tcctcgcaac	660
cttgogagga	ggagggcgtc	tggaagacca	gttgaattta	gctaagtttt	ctgagcgttt	720
tgattctttg	cgagaattat	ccgctaagct	tggttacgat	agcgtaggag	agactgggga	780
ttcttccac	gaggagtacg	acgacgaaga	agaggaaatc	aaaccgaaga	aaactacgaa	840
acgtggagct	aagaagagcc	gttcataagc	cttgccttta	agggttggtt	gttttacttc	900
tcataaatcc	aaatggttgc	gttgccaaaa	agtagtttgc	gttttcggat	gaggcgtaaa	960
tgocctctat	gaaagattgc	ttcgagagcg	gcacgcgcgt	ggagatcccg	aggaactctt	1020
ttcagatagc	aataagcata	gctgttccca	gaataaaaa	ggccgcagct	aggaacaaca	1080
agattttagat	agagcttggt	tagcaggttaa	actgggttat	atgttgcgtt	cggtgttaag	1140
ctcagaatac	ccaagtgtcc	tcacaggtgt	aataactgat	acaactccct	aagagcctct	1200
aatggatagg	ataagttccg	taatecatag	gccatagaag	ctaaacgaaa	cgattatt	1256

<210> 22

<211> 601

<212> DNA

<213> Chlamydia trachomatis

<400> 22

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tcgggttcgga	attcgtcttc	ttattccata	cgttaggctc	cgaagtttct	gtgatcgaag	120
caagctctca	aatccttgct	ttgaataatc	cagatatttc	aaaaaccatg	ttcgataaat	180
tcacccgaca	aggactccgt	ttcgtactag	aagcctctgt	atcaaatatt	gaggatatag	240
gagatcgcg	tcggttaact	atcaatggga	atgtcgaaga	atacagattac	gttcctcgat	300
ctataggagc	cogtttgaat	acagaaaata	ttggcttgga	taaagctggg	gttattttgt	360
atgaacgcgg	agtcacccct	accgatgcc	caatgcgcac	aaacgtacct	aacatttatg	420
ctattggaga	tatcacagga	aaatggcaac	ttgcccatgt	agcttctcat	caaggaatca	480
ttgcagcagc	gaatatagg	ggccataaag	aggaataatc	ttactctgct	gtccctctgt	540
tgatctttac	cttccctgaa	gtcgtctcag	taggcctctc	cccaacagca	gctcaacaac	600
a						601

<210> 23

<211> 270

<212> DNA

<213> Chlamydia trachomatis

<400> 23

acatctcctt	cttcgcttac	ttttttctgaa	aaatttgata	cagaagaaga	attcctcgca	60
caacttcgag	gaggagggcg	cttggaagac	cagttgaatt	tagctaagtt	ttctgagcgt	120
tttgattctt	tgcgagaatt	atccgcttaag	cttggttacg	atagcgatgg	agagactggg	180
gattttctca	acgaggagta	cgacgacgaa	gaagaggaaa	tcaaaccgaa	gaaaaactacg	240
aaacgtggac	gtaagaagag	cggttcataa				270

<210> 24

<211> 363

<212> DNA

<213> Chlamydia trachomatis

<400> 24

ttactctctc	aaaatccaaa	tggttgctgt	gccaaaaagt	agtttgctt	tccgatatg	60
gcgtaaatgc	gctgcatgaa	agattgcttc	gagagcggca	tcgcgtggga	gatcccgat	120
actttctctc	agatacgaat	aagcatagct	gttccacgaa	taaaaacggc	cgacgctagg	180
aacaacaaga	tttagataga	gcttggttag	caggtaaact	gggttatatg	ttgctgggag	240
tgtagttctc	agaataccca	agtgctctcc	aggttgtaat	actcgatata	cttccctaa	300
agcctctaatt	ggataggata	agttccgtaa	tccataggcc	atagaagcta	aacgaaacgt	360
att						363

<210> 25

<211> 696

<212> DNA

<213> Chlamydia trachomatis

<400> 25

gctcgtgccg	gcacgagcaa	agaaatccct	caaaaaatgg	ccattattgg	cggtgggtgtg	60
atcggttgccg	aattcgcttc	cttatcccat	acgttaggct	ccgaagtttc	tgtgatcgaa	120
gcaagctctc	aaatccttgc	tttgaataat	ccagatatatt	caaaaacat	gttcgataaa	180
ttcaccgcag	aaggactccg	ttctgacta	gaagcctctg	tatcaaatat	tgaggatata	240
ggagatcgcg	ttcggttaac	tatcaatggg	aatgtcgaa	aatacgatta	cgttctcgta	300
tcctatggac	gccgtttgaa	tacagaaaaat	attggcttgg	ataaagctgg	tgttatttgt	360
gatgaacgcg	gagtcacccc	taccgatgcc	acaatgcgca	caaacgtacc	taacatttat	420
gctattggag	atatcacagc	aaaatggcaa	cttgcccatg	tagcttctca	tcaaggaatc	480
attgcagcac	ggaatatagg	tgcccataaa	gaggaaatcg	attactctgc	tgctccctct	540
gtgatcttta	ccttccctga	agtcgcttca	gtaggcctct	ccccaacagc	agctcaacaa	600
catctccttc	ttcgcttact	ttttctga	aatttgatac	agaagaagaa	ttcctcgac	660
acttgcgagg	aggaggcgct	ctggaagacc	agttga			696

<210> 26

<211> 231

<212> PRT

<213> Chlamydia trachomatis

<400> 26

Ala	Arg	Ala	Gly	Thr	Ser	Lys	Glu	Ile	Pro	Gln	Lys	Met	Ala	Ile	Ile
1				5					10					15	
Gly	Gly	Gly	Val	Ile	Gly	Cys	Glu	Phe	Ala	Ser	Leu	Phe	His	Thr	Leu
				20				25					30		
Gly	Ser	Glu	Val	Ser	Val	Ile	Glu	Ala	Ser	Ser	Gln	Ile	Leu	Ala	Leu
				35				40				45			
Asn	Asn	Pro	Asp	Ile	Ser	Lys	Thr	Met	Phe	Asp	Lys	Phe	Thr	Arg	Gln
				50			55				60				
Gly	Leu	Arg	Phe	Val	Leu	Glu	Ala	Ser	Val	Ser	Asn	Ile	Glu	Asp	Ile
				65			70				75			80	
Gly	Asp	Arg	Val	Arg	Leu	Thr	Ile	Asn	Gly	Asn	Val	Glu	Glu	Tyr	Asp
				85						90				95	
Tyr	Val	Leu	Val	Ser	Ile	Gly	Arg	Arg	Leu	Asn	Thr	Glu	Asn	Ile	Gly
				100				105						110	
Leu	Asp	Lys	Ala	Gly	Val	Ile	Cys	Asp	Glu	Arg	Gly	Val	Ile	Pro	Thr
				115			120					125			
Asp	Ala	Thr	Met	Arg	Thr	Asn	Val	Pro	Asn	Ile	Tyr	Ala	Ile	Gly	Asp
				130			135				140				
Ile	Thr	Gly	Lys	Trp	Gln	Leu	Ala	His	Val	Ala	Ser	His	Gln	Gly	Ile
				145			150				155			160	
Ile	Ala	Ala	Arg	Asn	Ile	Gly	Gly	His	Lys	Glu	Glu	Ile	Asp	Tyr	Ser

```

165          170          175
Ala Val Pro Ser Val Ile Phe Thr Phe Pro Glu Val Ala Ser Val Gly
180          185          190
Leu Ser Pro Thr Ala Ala Gln Gln His Leu Leu Leu Arg Leu Leu Phe
195          200          205
Leu Lys Asn Leu Ile Gln Lys Lys Asn Ser Ser His Thr Cys Glu Glu
210          215          220
Glu Gly Val Trp Lys Thr Ser
225          230

```

<210> 27
 <211> 264
 <212> DNA
 <213> *Chlamydia pneumoniae*

```

<400> 27
atgagtc metaaaa ctctgctttt atgcaccccg tgaatat ttc cacagattta 60
gcagttatag ttggcaaggg accatgccc agaaccgaaa ttgtaaaaga agtttgggaa 120
tacattaaaa aacacaactg tcaggatcaa aaaaaataaac gtaatatcct tcccgatcgc 180
aatcttgcca aagtccttgg ctctagtgat cctatcgaca tgttccaaat gaccaaagcc 240
ctttccaaac atattgtaaa ataa 264

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<210> 28
 <211> 87
 <212> PRT
 <213> *Chlamydia pneumoniae*

```

<400> 28
Met Ser Gln Lys Asn Lys Asn Ser Ala Phe Met His Pro Val Asn Ile
1          5          10          15
Ser Thr Asp Leu Ala Val Ile Val Gly Lys Gly Pro Met Pro Arg Thr
20          25          30
Glu Ile Val Lys Lys Val Trp Glu Tyr Ile Lys Lys His Asn Cys Gln
35          40          45
Asp Gln Lys Asn Lys Arg Asn Ile Leu Pro Asp Ala Asn Leu Ala Lys
50          55          60
Val Phe Gly Ser Ser Asp Pro Ile Asp Met Phe Gln Met Thr Lys Ala
65          70          75          80
Leu Ser Lys His Ile Val Lys
85

```

<210> 29
 <211> 369
 <212> DNA
 <213> *Chlamydia pneumoniae*

```

<400> 29
atgccacgca tcattggaat tgatattcct gcaaaagaaa agttaaaaat aagtcctgaca 60
tatatttatg gaataggatc agctcgttct gatgaaatca ttaaaaagtt gaagttagat 120
cctgaggcaa gagcctctga attaactgaa gaagaagtag gacgactgaa ctctctgcta 180
caatcagaat ataccgtaga aggggatttg cgacgtcgtg ttcaatcgga tatcaaaaga 240
ttgactcgcca tcattcttta tcgaggtcag agacatagac ttctttacc agtaagagga 300
caacgtacaa aaactaattc tcgtactcga aaaggtaaaa gaaaaacagt cgcaggtaag 360
aagaaataa 369

```

<210> 30
 <211> 122
 <212> PRT

<213> *Chlamydia pneumoniae*

<400> 30

```

Met Pro Arg Ile Ile Gly Ile Asp Ile Pro Ala Lys Lys Lys Leu Lys
 1           5           10           15
Ile Ser Leu Thr Tyr Ile Tyr Gly Ile Gly Ser Ala Arg Ser Asp Glu
 20           25           30
Ile Ile Lys Lys Leu Lys Leu Asp Pro Glu Ala Arg Ala Ser Glu Leu
 35           40           45
Thr Glu Glu Glu Val Gly Arg Leu Asn Ser Leu Leu Gln Ser Glu Tyr
 50           55           60
Thr Val Glu Gly Asp Leu Arg Arg Val Gln Ser Asp Ile Lys Arg
 65           70           75           80
Leu Ile Ala Ile His Ser Tyr Arg Gly Gln Arg His Arg Leu Ser Leu
 85           90           95
Pro Val Arg Gly Gln Arg Thr Lys Thr Asn Ser Arg Thr Arg Lys Gly
100           105           110
Lys Arg Lys Thr Val Ala Gly Lys Lys Lys
115           120

```

<210> 31

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in the lab

<400> 31

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Cys Ser Phe Ile Gly Gly Ile Thr Tyr Leu
 1           5           10

```

<210> 32

<211> 53

<212> PRT

<213> *Chlamydia trachomatis*

<400> 32

```

Leu Cys Val Ser His Lys Arg Arg Ala Ala Ala Val Cys Ser Phe
 1           5           10           15
Ile Gly Gly Ile Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile
 20           25           30
Leu Phe Val Asn Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Thr
 35           40           45
Lys Ala Asn Met Gly
50

```

<210> 33

<211> 161

<212> DNA

<213> *Chlamydia trachomatis*

<400> 33

```

atctttgtgt gtctcataag cgcagagcgg ctgcggctgt ctgtagcatc atcggaggaa      60
ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac aaaatgctgg      120
caaaaccgtt tctttcttcc caaactaaag caaatatggg a                          161

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<210> 34

```

<211> 53
<212> PRT
<213> Chlamydia trachomatis

<400> 34
Leu Cys Val Ser His Lys Arg Arg Ala Ala Ala Val Cys Ser Ile
 1           5           10           15
Ile Gly Gly Ile Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile
          20           25           30
Leu Phe Val Asn Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr
          35           40           45
Lys Ala Asn Met Gly
 50

<210> 35
<211> 55
<212> DNA
<213> Chlamydia pneumoniae

<400> 35
gatatacata tgcataccca tcaccatcac atgagtcaaa aaaaataaaa actct      55

<210> 36
<211> 33
<212> DNA
<213> Chlamydia pneumoniae

<400> 36
ctcgaggaat tcttatttta caatatgttt gga      33

<210> 37
<211> 53
<212> DNA
<213> Chlamydia pneumoniae

<400> 37
gatatacata tgcataccca tcaccatcac atgccacgca tcattggaat gat      53

<210> 38
<211> 30
<212> DNA
<213> Chlamydia pneumoniae

<400> 38
ctcgaggaat tcttattttt ttttacctgc      30

<210> 39
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 39
Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys Val Phe Gly Thr
 1           5           10           15

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<210> 40
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> made in the lab

<400> 40
 Lys Arg Asn Ile Leu Pro Asp Ala Asn Leu Ala Lys Val Phe Gly Ser
 1 5 10 15

<210> 41
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> made in the lab

<400> 41
 Lys Glu Tyr Ile Asn Gly Asp Lys Tyr Phe Gln Gln Ile Phe Asp
 1 5 10 15

<210> 42
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> made in the lab

<400> 42
 Lys Lys Ile Ile Ile Pro Asp Ser Lys Leu Gln Gly Val Ile Gly Ala
 1 5 10 15

<210> 43
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> made in the lab

<400> 43
 Lys Lys Leu Leu Val Pro Asp Asn Asn Leu Ala Thr Ile Ile Gly
 1 5 10 15

<210> 44
 <211> 509
 <212> DNA
 <213> Chlamydia

<400> 44
 ggagctcgaa ttcggcacga gagtgccat tgttttcgag gctttgtctg atgatagcga 60
 taccgtacgt gagattgctg tacaagtagc tgttatgtat ggttctagtt gcttactgcg 120
 cgccgtgggc gatttagcga aaaatgattc ttctattcaa gtacgcacga ctgcttatcg 180

```

tgctgcagcc  gttgtggaga  tacaagatct  tgtgcctcat  ttacgagttg  tagtccaaaa  240
tacacaatta  gatggaaacg  aaagaagaga  agcttggaga  tctttatgtg  ttcttactcg  300
gcctcatagt  ggtgtattaa  ctggcataga  tcaagcttta  atgacctgtg  agatgttaaa  360
ggaatatcct  gaaaagtgtg  cggaagaaca  gattcgtaga  ttattggctg  cagatcatcc  420
agaagtgcag  gtactacttt  tacagatcat  tctgagagga  ggtagagtat  tccggtcatc  480
ttctataatg  gaatcggttc  tctgtccgg  509

```

```

<210> 45
<211> 481
<212> DNA
<213> Chlamydia

```

```

<220>
<221> unsure
<222> (23)
<223> n=A,T,C or G

```

```

<400> 45
gatccgaatt  cggcagcagg  cantatttac  tcccaacatt  acggttccaa  ataagcgata  60
aggtcttctta  ataaggaaagt  taatgtaaga  ggctttttta  ttgcttttctg  taaggtagta  120
ttgcaaccgc  acgcgattga  atgatacgca  agccatttcc  atcatggaaa  agaacccttg  180
gacaaaaata  caaaggaggt  tcaactcctaa  ccagaaaaag  ggagagttag  ttccatggg  240
ttttctctat  atacaccgtt  ttacacacaa  taggagccgc  gtctagtatt  ttggaatacaa  300
attgtcccca  agcgaaatttt  gttcctgttt  cagggatttc  tcttaattgt  tctgtcagcc  360
atccgcctat  ggtaacgcaa  ttagctgtag  taggaagatc  aactccaaac  aggtcataga  420
aatcagaaag  ctcataggtg  cctgcagcaa  taacaacatt  cttgtctgag  tgagcgaaatt  480
g  481

```

```

<210> 46
<211> 427
<212> DNA
<213> Chlamydia

```

```

<220>
<221> unsure
<222> (20)
<223> n=A,T,C or G

```

```

<400> 46
gatccgaatt  cggcagcagn  tttttcctgt  tttttcttag  tttttagtgt  tcccgagaca  60
ataacacaga  tcaagaacg  gccattcagt  ttaggctctg  actcaacaaa  acctatgtcc  120
tctaagccct  gacacattct  ttgaacaacc  ttatgccctg  gttcgggata  agccaacctc  180
cgcccccga  acatacaaga  aacctttact  ttatttctct  tctcaataaa  ggctctagct  240
tgctttgtct  tctgaagaaa  gtcgtttatc  tcgatattag  gcttaagctt  aacctctttg  300
atacgcactt  ggtgctgtgc  ttcttacta  tcttttctct  ttttagttat  tctgtaacga  360
tacttccctg  agtccatgat  ttgacacaca  ggaggctctg  agtttgaaac  aacctctgtc  420
ggaattc  427

```

```

<210> 47
<211> 600
<212> DNA
<213> Chlamydia

```

```

<220>
<221> unsure
<222> (522)
<223> n=A,T,C or G

```

```

<400> 47
gatccgaatt cggcacgaga tgcttctatt acaattgggt tggatcgga aaaagcttac 60
cagcttattc tagaaaagtt gggagatcaa attcttgggt gaattgctga tactattggt 120
gatagtcacg tccaagatat tttagacaaa atcacaacag accctctctc aggtttgttg 180
aaagctttta acaactttcc aatcactaat aaaattcaat gcaacgggtt attcactccc 240
aggaacattg aaactttatt aggaggaact gaaataggaa aattcacagt cacaccctaa 300
agctctggga gcatgttctt agtctcagca gatattatg catcaagaa ggaaggcggc 360
gttgctctag ctttggtagc agaaggtgat tctaagccct acgcgattag ttatgggatac 420
tcacacggcg ttccataatt atgtagtcta agaaccagaa ttattaatatc aggattgact 480
ccgacaacgt attcattacg tgtaggcggt ttagaacgag gngtggtagt gggttaatgcc 540
ctttctaatt gcaatgatat tttaggaata acaaatcttc taatgtatct tttttggagg 600

```

```

<210> 48
<211> 600
<212> DNA
<213> Chlamydia

```

```

<400> 48
ggagctcgaa ttccggcaga gctctatgaa tatccaattc tctaaactgt tcggataaaa 60
atgagtcagg aattaggttc acactattct tttttgtttc gcaaatgatt gattttaaat 120
cgtttgatgt gtatactatg tegtgtgaagc ctttttgggt actctcgaca ctgaccccc 180
atccagaaga taacttggtt tgcgggtcta ggtcagcaag taacactttt tccctctaaa 240
attggggcaa gttgcattcc acgttttagag aaagtgttgt ttttccagtt ttccctctaa 300
aagagcaaaa aactaagggt tgcataatcaa ctccaacgtt agagtaagtt atctattcag 360
ccttgaaaaa catgtctttt ctagacaaga taagcataat caaagccttt tttagcttta 420
aactgttatt ctctaatttt tcaagaacag gagagtctgg gaataatcct aaagagtttt 480
ctattgtttg aagcagtcct agaattatgt agacactttt atggtagagt tctaaggagg 540
aatttaagaa agttactttt tccttgttta ctctgtattt taggtctaat tcggggaat 600

```

```

<210> 49
<211> 600
<212> DNA
<213> Chlamydia

```

```

<400> 49
gatccgaatt cggcacgaga tgcttctatt acaattgggt tggatcgga aaaagcttac 60
cagcttattc tagaaaagtt gggagatcaa attcttgggt gaattgctga tactattggt 120
gatagtcacg tccaagatat tttagacaaa atcacaacag accctctctc aggtttgttg 180
aaagctttta acaactttcc aatcactaat aaaattcaat gcaacgggtt attcactccc 240
aggaacattg aaactttatt aggaggaact gaaataggaa aattcacagt cacaccctaa 300
agctctggga gcatgttctt agtctcagca gatattatg catcaagaa ggaaggcggc 360
gttggtctag ctttggtagc agaaggtgat tctaagccct acgcgattag ttatgggatac 420
tcacacggcg ttccataatt atgtagtcta agaaccagaa ttattaatatc aggattgact 480
ccgacaacgt attcattacg tgtaggcggt ttagaacgag ggtgtggtagt gggttaatgcc 540
ctttctaatt gcaatgatat tttaggaata acaaatactt ctaatgtatc tttttggagg 600

```

```

<210> 50
<211> 406
<212> DNA
<213> Chlamydia

```

```

<400> 50
gatccgaatt cggcacgagt tcttagcttg cttaattacg taattaaacca aactaaaggg 60
gctatacaat agcttattca gcttttcatt agttaaacga tctttctcag ccatgactca 120
tctatttgct ttcagctata aaaatacttc ttaaaacttg atatgctgta atcaaatcat 180
cattaaccac aacataatca aattcgctag cggcagcaat tctgcagcag catgctctca 240
atctttcttt ctctcggaat tctttctctg aatcccgagc attcaaacgg cgtctcaagt 300
cttcttgaga gggagcttga ataaaaatgt gactgcgcgc atttgctctc tcagagccaa 360

```


agctcctgtg acatcaatca cggctatgca gtctcgtgcc gaattc

406

<210> 51
<211> 602
<212> DNA
<213> Chlamydia

<400> 51
gatccgaatt cggcacgaga tattttagac aaaatcacaa cagacccttc tctagggttg 60
ttgaaagctt ttaaccaact tccaatcact aataaaatc aatgcaacgg gttattcact 120
cccaggacaa ttgaaacttt attaggagga actgaaatag gaaaattcac agtcacaccc 180
aaaagctctg ggagcatggt cttagtctca gcagatatta ttgcatcaag aatggaaggc 240
ggcgttggtc tagctttggt acgagaaggt gattctaacg cctacgcgat tagttatgga 300
tactcatcag cgtttcctaa tttatgtagt ctaagaacca gaattattaa tacaggattg 360
actccgacaa cgtattcatt acgtgtaggc gggttagaaa cgggtgtggt atgggttaat 420
gccctttcta atggcaatga tattttagga ataacaata cttctaagt atcttttttg 480
gaggtaatac ctcaaacaaa cgtttaaaca atttttattg gatttttctt atagggttta 540
tatttagaga aaaaagttcg aattacgggg ttgttatgc aaaataaact cgtgccgaat 600
tc 602

<210> 52
<211> 145
<212> DNA
<213> Chlamydia

<400> 52
gatccgaatt cggcacgagc tcgtgccgat gtgttcaaca gcattccatag gatgggcagt 60
caaatatact ccaagtaatt cttttctctt ttccaacaac tccttaggag agcgttggat 120
aacattttca gctcgtgcgc aattc 145

<210> 53
<211> 450
<212> DNA
<213> Chlamydia

<400> 53
gatccgaatt cggcacgagg taatcggcac cgcactgctg acactcatct cctcagagtc 60
gatcaaaccc acacttggga caagtaccta caacataacg gtcgcctaaa aactccctt 120
cttcctcaga atacagctgt tcggtcacct gattctctac cagtcgcgtt tcttcgaagt 180
ttcagataga atcttgacaa atagcaggat gataagcgtt cgtagttctg gaagaagaat 240
ctacagaaat tcccaatttc ttgaagggtt ctttatgaag cttatgatgc atctcgacat 300
attcttgata ccccatgctt gccaacctctg cattaagggt aattgcgatt ccgtattcat 360
cagaaccaca aatatacaaa acctctttgc cttgtagtct ctgaaaaacg gcataaacat 420
ctgcaggcaa ataagctcgt tgcgaattc 450

<210> 54
<211> 716
<212> DNA
<213> Chlamydia

<400> 54
gatcgaatt cggcacgagc ggcacgagtt ttctgatagc gatttacaat cctttattca 60
acttttgctt agagaggcac actatactaa gaagtctctt ggggtgtgtg cacagtccgt 120
tcgtcagggtt attctgctag aggggttagg gaaaaaaccc ttattactat gaccatgcgc 180
atgtggaatt acattccata gactttcgca tcattcccaa catttacaca gctctacacc 240
tcttaagaag aggtgacgtg gattgggttg ggcagccttg gcaccaaggg attccttttg 300
agcttcggac tacctctgct ctctacaccc attaccctgt agatggcaca ttctggctta 360
tctttaatcc caaagatcct gtactttcct ctctatctaa tcgtcagcga ttgattgtcg 420

```

ccatccaaaa ggaaaaaactg gtgaagcaag ctttaggaac acaatatcga gtgactgaaa 480
gctctccatc tcacagagga atcatagctc atcaagaagc ttctactcct ttctctggga 540
aaatctcttt gatatatccc aataatatta cgcgctgtca gcgtttggcc gaggtatcca 600
aaaaatgatg gacaaggagc acgctaattt tgtacatacc ccaaaatcaa tcagccatct 660
aggcaaatgg aatatcaaa gtaaacagat acaactgggg atctcgtgcc gaattc 716

```

<210> 55

<211> 463

<212> DNA

<213> Chlamydia trachomatis

<400> 55

```

tctcaaatcc ttgctttgaa taatccagat atttcaaaaa ccatgttcga taaattcacc 60
cgacaaggac tcgctttcgt actagaagcc tctgtatcaa atattgagga tataggagat 120
cgcgcttcgt taactatcaa tgggaatgtc gaagaatacg attacgttct cgtatctata 180
ggacgcgctt tgaatacaga aatatattgc ttggataaag ctggtgttat ttgtgatgaa 240
cgcgagtgca tcctacccga tgcacaaatg cgacacaaag tactatacat ttatgctatt 300
ggagatatca caggaaaaatg gcaacttgcc catgtgacct ctcatcaagg aatcattgca 360
gcacggaata taggtggcca taagaggaaa atcgatctac ctgctgtccc ttctgtgatc 420
tttaccttcc ctgaagtcgc ttcagtaggc ctctcccaaa cag 463

```

<210> 56

<211> 829

<212> DNA

<213> Chlamydia trachomatis

<400> 56

```

gtactatggg atcattagtt ggaagacagg ctcgggattt ttctggtaaa gccgttgttt 60
gtggagaaga gaaagaatac tctctagcag actttcgttg taagtatgta gtgctcttct 120
tttatcccaa agattttacc tatgtttgtc ctacagaatt acatgctttt caagatagat 180
tggttagatt tgaagagcat ggtgcagctg tcttggtttg ctcggttgac gacattgaga 240
cacattcttt ttggctcact gtgacgagag atgcaggagg gatagagga acagaatact 300
ctctgttagc agacccctct tttaaaaat cagaagcttt tgggtgtttg aatcctgaag 360
gatcgctcgc tttaaagact actttcctta tcgataaaca tggggttatt cgtcatgcgg 420
ttatcaatga tcttctttaa gggcgcttcc ttgacagagg attgcgtatt ttgattcatc 480
tgatcttctt tgagaaccac ggaatggttt gtccagctaa ctggcgcttc ggagagcgtg 540
gaatggtgcc tcttgaagag ggaataaaaa aatacttcca gacgatggat taagcatctt 600
tgaaagtaag aaagtctgac agatcttgat ctgaaaaagag aagaaggctt ttaatttttc 660
tgcagagagc cagcgaggct tcaataatgt tgaaagtctc gacaccaggc aatgctaagg 720
gcacgatatt agttagtaa gcttgagat taaggaaatg aaggccaaag aaatagctat 780
caataaagaa gccctcttcc ttgactctaa agaatagtat gcgtatcc 829

```

<210> 57

<211> 1537

<212> DNA

<213> Chlamydia trachomatis

<400> 57

```

acatcaagaa atagcggact cgccttttagt gaaaaaagct gaggagcaga ttaatcaagc 60
acaacaagat attcaaacga tcacacctag tgggtttggat attcctatcg ttggtccagc 120
tgggtcagct gcttcgcgag gaagtgcggc agggagcgtt aaatcctcta acaattcagg 180
aagaatttcc ttgttgcttg atgatgtaga caatgaaatg gcagcgattg caatgcaagg 240
ttttcgatct atgatcgaac aatttaattgt aaacaatctc gcaacagcta aagagctaca 300
agctatgtgag gctcagctga ctgcgatgtc agatcaactg gttggtgcgg atggcgagct 360
ccagccgcaa atacaagcaa tcaaatgtgc tcttgcccaa gctttgaaac aaccatcagc 420
agatggttta gctacagcta tgggacaagt ggtcttttga cgtgccaaag ttggagagg 480
ctccgcagga acagctggca ctgtccagat gaatgtaaaa cagctttaca agacagcgtt 540
ttcttcgact tcttcagct cttatgcagc agcactttcc gatggatatt ctgcttcaaa 600

```

```

aacactgaac  tctttatatt  cggaaagcag  aagcggcgctg  cagtcagcta  ttatgtaaac  660
tgcaaatccc  gcgctttcca  gaagcggttc  tcgttctggc  atagaaagtc  aaggacgcag  720
tgcagatgct  agccaaagag  cagcagaaac  tattgtcaga  gatagccaaa  cgttagtgta  780
tgatatagc  cgcttacagg  ttctggattc  tttgatgtct  acgatttgta  gcaatccgca  840
agcaaatcaa  gaagagatta  tgcagaagct  caccgcctct  attagcaaac  ccccacatt  900
tgggtatcct  gctgttcaga  attctgtgga  tagcttgca  aagtgttgctg  cacaattgga  960
aagagagttt  gttgatgggg  aacgtagtct  cgcagaatct  caagagaatg  cgttttagaaa  1020
acagcccgct  ttcattcaac  aggtgttggt  aaacattgct  tctctattct  ctggttatct  1080
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ttagtcccaa  aagaagaaaa  tatataaaag  aaaaaactcc  taattcattt  aaaaagtgtc  1260
cggcagactt  cgtggaaaat  gtctgtaaag  ctggagggga  atcagcagaa  agatgcaaga  1320
tatccagaaa  aaaaggctca  ggctcgtgcc  gaattcgcca  cgagactacg  aaagaaaggt  1380
cttttcttct  ggaatctgtc  attggaatcg  cgtaaagact  aaagttcgcc  aacacagcgt  1440
ctgtctctct  tttaggtttc  ttgcgcgaga  aaaattttct  caagtaacaa  gaagattttc  1500
ttttacagcc  ggcacccgcc  ttctcgcgaa  gtataaac  1537

```

<210> 58

<211> 463

<212> DNA

<213> Chlamydia trachomatis

<400> 58

```

ttctcaaatcc  ttgctttgaa  taatccagat  atttcaaaaa  ccatgttcga  taaattcacc  60
cgacaaggac  tcogtttctg  actagaagcc  tctgtatcaa  atattgagga  tataggagat  120
cggcttcgggt  taactatcaa  tgggaatgtc  gaagaatacg  attacgtttt  cgtatctata  180
ggacgcctgt  tgaatacaga  aaatatggc  ttggataaag  ctggtgttat  ttgtgatgaa  240
cggggagtca  tccctaccca  tggccacaatg  cgcacaaaag  tacctaaat  ttatgtctatt  300
ggagatatca  caggaaaatg  gcaacttgcc  catgtagact  ctcatcaagg  aatcatgtca  360
gcacggaata  taggtggcca  taaagaggaa  atcgattact  ctgctgtccc  ttctgtgact  420
tttaccctcc  ctgaagtcgc  ttcaagtaggc  ctctcccacaa  cag  463

```

<210> 59

<211> 552

<212> DNA

<213> Chlamydia trachomatis

<400> 59

```

acattctctc  tgctcctcgc  ggccatccac  aaattgaggt  aaccttcgat  attgatgcca  60
acggaatttt  acagctttct  gctaaagatg  ctgctagtgg  acgcgaaaca  aaaaatccga  120
ttgagcagaa  cctctggatta  aaagaagatg  aaattcaaca  aatgatccgc  gatgcagagc  180
ttcataaaga  ggaagacaaa  caacgaaaaa  aagcttctga  tggcaaaaaat  gaagccgatg  240
gaatgatctt  tagagctcgaa  aaagctgtga  aagattacca  cgcacaaaat  ctgcagaaac  300
ttgttaaaga  aattgaagag  catattgaga  aagtacgcca  agcaatcaaa  gaagatgctt  360
ccacaacagc  tatcaaaagca  gcttctgatg  agttgagtag  ctgtatgcaa  aaaaatcgga  420
aagctatgca  ggctcaatcc  gcatccgcag  cagcatcttc  tgcagcgaat  gctcaaggag  480
ggccaaacat  taactccgaa  gatctgaaaa  aacatagttt  cagcacacga  cctccagcag  540
gaggaagcgc  ct  552

```

<210> 60

<211> 1180

<212> DNA

<213> Chlamydia trachomatis

<400> 60

```

atcttagcgg  taaaactgct  tactgggtcag  ataaaaacca  tacagaagca  acacgtactt  60
cttttaggag  aaaaaatcta  taatgctaga  aaaatccgta  gtaaggatca  cttctctcta  120
acaacttttt  catcttggat  agagtttagtt  ttgaagacta  agtcttctgc  ttacaatgct  180

```

```

cttgcataatt acgagctttt tataaacctc cccaaccaa ctctacaaaa agagtttcaa 240
tcgatccctc ataaatccgc atatatattt gcgcctagaa aaggcgattt aaaaaccaag 300
gtcgtatgtga tagggaaagt atgtggaatc tcgtgccgaa ttcggcacga gcggcacgag 360
gatgtagagt aattagttaa agagctgcac aattatgaca aagcatggaa aacgcatttc 420
tggtatccaa gagacttaac atttagctaa tgcgtattct ttgggtgaa cgtatagata 480
tttaaaacag tgtcctactg tgcgttttca tcaaacgggt gatgtgtctg ttaaattagg 540
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acgaggagcg gactttgttg gtacgcaga ctgtgtagaa aaaatcaaag gtggatgggt 720
tgacttcgat gttgcgggtg ccactccgca tatgatgaga gaggctggaa agctaggaaa 780
agtttttagt ccaagaaacc ttatgcctac gcctaagacc ggaactgtaa caacagatgt 840
ggtttaaaat attgcggaac tgcgaaaaag taaaattgaa tttaaagctg actcagctgg 900
tgtatgcaac gtccgaggtg cgaagctttc tttcgtatgt gcgcaaatca aagaaaatgt 960
tgaacgcttg tgtgcagcct tagttaaagc taagcccgca actgctaaag gacaatattt 1020
agttaatttc actatttctc cgaccatggg gccaggggtt accgtggata ctaggagggt 1080
gattgcgtta taattctaag tttaaaggag aaaaatgaaa agtagaaaa agttgtctgt 1140
tcgcgaggtt gaagaaaaga taaccgcttc tcggcacgag 1180

```

<210> 61

<211> 1215

<212> DNA

<213> Chlamydia trachomatis

<400> 61

```

attacagcgt gtgcaggtaa cgcacatcatt gcatgatgct tttgatggca ttgatgcgcg 60
attccttata ggggtcagttc ctgagggccc aggaatggag agaagagatc ttctaaagaa 120
aaatggggag attgttgcta cgcaaggaaa agctttgaac acaacagcca agcgggatgc 180
aaagattttt gttgttggga accctgtgaa taccgaattgc ttgatagcaa tgaatcatgc 240
tcccagatta ttgagaaaga actttcatgc gatgctacga ttggaccaga actgatatga 300
tagcatgtta tcgcataagag cagaagtacc tttatcggct gtatcacaag ttgtggtttg 360
gggaaatcac tcgcaccaac aagtgcctga ttttacycaa gctctgatga atgaccgtcc 420
tatcgacagc acgatagcgg atcgtgatgt gttagagaat attatggttg ctctgtatac 480
gagtcgtggt agtcagtaaa ttgaagcagc agggaaagct tcggcagcgt ctgcagcacg 540
agcttttagc gaggtcgtct gatcaatata tcagccaaaa gaaggactcg tggcgaaatc 600
ggcagcagta tcgaaattgc aggcattttc agtgaatggt cgtatgctta taaactacgt 660
ggtacagact tgagctctca aaagtgtgct acagattctt acatcgaga ccttattctc 720
aagaatatct actcctctca actatttgga tccctaaaac aagaaaaagg ttaacgattt 780
agttactctg aatatgagga ttttgactgg gaaggcgaca ctcttttgca ccttccaaaa 840
gaaaattact tcaattatga aatgcatggt cggctcatca cccgagatcc gtcttccagc 900
gtttcccatc ctggaaactt ccttggtatc atcgaaaaaa tagaccactc tgaccacta 960
ggcgttcagt cagttgaact ccttctcatt ttogaattcg atgaaacgt ccatccattt 1020
aaaaatcagg acttccccc cctgtgtaac taattggggt atctctcgtt gaattttttc 1080
tgccctctc gcggttatac ttatggggca gacctgtctg ctccggcccg agagttcaag 1140
actcttgtca aagcgtttaca cgtgcggga atcgaaagtc tctcgtatgt cgttttcaat 1200
catcacgctc ttgaa 1215

```

<210> 62

<211> 688

<212> DNA

<213> Chlamydia trachomatis

<400> 62

```

gtggatccaa aaaagaatct aaaaagccat acaaagattg cgttacttct tgcgatgcct 60
ctaacacttt atcagcgtca tcttttgaaa gcatctcaat gagcgtcttt tcttctctag 120
catgcgcgac atccgcttct tcatgttctg tgaatatatc atagtcttca ggtatggaaa 180
atccaaagta ctcaagtcaat ccacgaattt tctctctagc gatcgtgga atttgactct 240
cataagaata caaagcagcc actcctgcag ctaaaagatc tctgtacac caccgatga 300
aagtagctac tttcgtttt gctgcttcac taggctcatg agcctctaac tcttctggag 360

```

```

taactcctag agcaaacaca aactgcttcc acaaatcaat atgattaggg taaccgttct 420
cttcctccat caagttatct aacaataact taocgcgcctc taaatcatcg caacgactat 480
gaatcgcaga taaatattta ggaaaggctt tgatatgtaa ataatagctc ttggcagcag 540
cctgtaattg ctcttttagta agctccccctc tcgaccattt cacataaaac gtgtgtttcta 600
gcattgctct attttgaata attaaatcta actgatctaa aaaattcata aacacctcca 660
toattttttt tcttgactcc acgtaacc 688

```

<210> 63

<211> 269

<212> DNA

<213> *Chlamydia trachomatis*

<400> 63

```

atgttgaat cacacaaagt gttcctaaat atgtctacgt aggatctccc tatcctgttg 60
aaattactgc tacaggtaaa agggatttgt ttgatgttat cattactcag caattaccat 120
gtgaagcaga gttcgtacgc agtgateccag cgacaactcc tactgctgat ggttaagctag 180
tttggaaaat tgaccgctta ggacaaggcg aaaagagtaa aattactgta tgggtaaaac 240
ctcttaaaaga aggttctgc tttacagct 269

```

<210> 64

<211> 1339

<212> DNA

<213> *Chlamydia trachomatis*

<400> 64

```

cttttattat ggctctctggg gatgatgtca acgatatcga cctgctatct cgaggagatt 60
ttaaaattgt tatacagacg gctccagagg agatgcctgg attagcggac tttttggctc 120
ccccgcgcaa ggcattctggg attctctccg cctggggaagc tgggtgagctg cgtttcaaac 180
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cacatagaga gtttctcccg taattgcgct agctagggga gagactaaga aggtcgtctc 300
tgcgcctact tgctcagctt ccattggaga aggtagtgtga gccacgtctt ggtagttaac 360
caccattctc tcaataaact caatagcttt tctctcacgg ctagctaatt gccctgcgca 420
gatagtattc actcggactc cccaacgtcg gccggtctcc caagccagta cttttgtatc 480
actttctaaa gcagcttttg ctgcgttcat tctctcgcca taccctggaa cagcacgcat 540
ggaagcaaga taagttagag agatggtgct agctcctgca tctcataattg ggccaaaatg 600
agagagaagg ctgataaagg agtagctgga tgtacttaag gcggcaagat agcctttacg 660
agaggtatca agtaatgggt tagcaatttc cggactgttt gctaaagagt gaacaagaat 720
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aagatctttg taacgtttat tttccaaaat ttctcgagga atatcttctg ggggtgcgaa 840
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aaagagtttc ctgtcaaat tcttatatgg gttagagtaa tcaactgttt tcaagtgtat 1260
tatgtttatt ttaaaataat ttgttttaac aactgtttaa tagtttttaat ttttaagtg 1320
tgaaaaacag gttttatat 1339

```

<210> 65

<211> 195

<212> PRT

<213> *Chlamydia trachomatis*

<400> 65

Met Gly Ser Leu Val Gly Arg Gln Ala Pro Asp Phe Ser Gly Lys Ala

5

10

15

Val Val Cys Gly Glu Glu Lys Glu Ile Ser Leu Ala Asp Phe Arg Gly
 20 25 30
 Lys Tyr Val Val Leu Phe Phe Tyr Pro Lys Asp Phe Thr Tyr Val Cys
 35 40 45
 Pro Thr Glu Leu His Ala Phe Gln Asp Arg Leu Val Asp Phe Glu Glu
 50 55 60
 His Gly Ala Val Val Leu Gly Cys Ser Val Asp Asp Ile Glu Thr His
 65 70 75 80
 Ser Arg Trp Leu Thr Val Ala Arg Asp Ala Gly Gly Ile Glu Gly Thr
 85 90 95
 Glu Tyr Pro Leu Leu Ala Asp Pro Ser Phe Lys Ile Ser Glu Ala Phe
 100 105 110
 Gly Val Leu Asn Pro Glu Gly Ser Leu Ala Leu Arg Ala Thr Phe Leu
 115 120 125
 Ile Asp Lys His Gly Val Ile Arg His Ala Val Ile Asn Asp Leu Pro
 130 135 140
 Leu Gly Arg Ser Ile Asp Glu Glu Leu Arg Ile Leu Asp Ser Leu Ile
 145 150 155 160
 Phe Phe Glu Asn His Gly Met Val Cys Pro Ala Asn Trp Arg Ser Gly
 165 170 175
 Glu Arg Gly Met Val Pro Ser Glu Glu Gly Leu Lys Glu Tyr Phe Gln
 180 185 190
 Thr Met Asp
 195

<210> 66
 <211> 520
 <212> DNA
 <213> Chlamydia

<400> 66
 gatccgaatt cggcacgagg aggaatggaa gggccctccg attttaaatc tgctaccatg 60
 ccattcacta gaaactccat aacagcggtt ttctctgatg gcgagtaaga agcaagcatt 120
 tgatgtaaat tagcgcaatt agagggggat gaggttactt ggaaatataa ggagcgaagc 180
 gatgaaggag atgtatttgc tctggaagca aaggtttctg aagctaacag aacattgcgt 240
 cctccaacaa tcgcttgagg attctggctc atcagttgat gctttgcctg aatgagagcg 300
 gacttaagtt tcccatcaga gggagctatt tgaattagat aatcaagagc tagatccttt 360
 attgtgggat cagaaaaatt acttgtagac gcacgcagaa tttcgtcaga agaagaatca 420
 tcacgaacg aatttttcaa tcttcgaaaa tcttctccag agacttcgga aagatctctt 480
 gtgaaacgat cttcaagagg agtatcgctt ttttctctctg 520

<210> 67
 <211> 276
 <212> DNA
 <213> Chlamydia

```

<400> 67
gatccgaatt cggcacgagg tattgaagga gaaggatctg actcgatcta tgaatcatg 60
atgccttatct atgaagttat gaataatggat ctagaaacac gaagatcttt tgcggtacag 120
caagggcact atcaggaccc aagagcttca gattatgacc tcccacgtgc tagcgactat 180
gatttgccta gaagccata tctactcca ctttgcctt ctagatatca gtcacagaat 240
atggatgtag aagcagggtt cgtgaggca gtttat 276

```

```

<210> 68
<211> 248
<212> DNA
<213> Chlamydia

```

```

<400> 68
gatccgaatt cggcacgagg tgttcaagaa tatgtccttc aagaatgggt taaattgaaa 60
gatctaccgg tagaagattt gctagaaaaa cgatatcaga aattccgaac gatagggtcta 120
tatgaaacttt ctctgaaaag cgattctgag gcataagaag catttagttt tattcggttt 180
ttctctttta tccatattag ggctaacgat aacgtctcaa gcagaaattt tttctctagg 240
tcttattg 248

```

```

<210> 69
<211> 715
<212> DNA
<213> Chlamydia

```

```

<220>
<221> unsure
<222> (34)
<223> n=A,T,C or G

```

```

<400> 69
gatccgaatt cggcacgaga aggtagatcc gatntcagca aaagtgtccc taaaggaaga 60
ttccttcggt atcctgcagc aaataaggtg gcacactcca tctcgacagc tttagcttt 120
attttcatat agttttcgac ggaaactcttt attaaactcc caaaaccgaa ttttagctgt 180
gtgggtgatg cctatatggt aagggaggtt ttgtgcttcg agaatttgg tgatcatttt 240
ttgtacgaca aaattagcta atgcagggac ctctgggggg aagtatgcat ctgatgttcc 300
atctttttcg atgctagcaa cagggacaaa ataactctct atttggtagt gggatcttaa 360
gcctccgcac atgcccacaa tgatcgctgc tgtagcattg ggaaggaaag aacacagatc 420
tacggttaaga gctgctcctg gagagcctaa tttaaaatcg atgattgagg tgtgaatttg 480
aggcgatgct gctgcggaac acatggatcc tcgagaacaa gggacatgat agatttcagc 540
gaaaacatcc acggtataac cmaaaattag taagaaggag atagggtctg aactcttgaa 600
tggtagagcc ggtatagcgc tctagcatgt cacaggcgat tgtttcttcg ctgatttttt 660
tatgttgatg ggtcataaat cacagatatt ataattggtta gagaactctt ttttc 715

```

```

<210> 70
<211> 323
<212> DNA
<213> Chlamydia

```

```

<400> 70
gatccgaatt cggcacgagc agaacgtaaa cagcacactt aaaccgtgta tgaggtttaa 60
cactgtttgg caagcaaaaca accattctct ttccacatc gttcttacc aacactctga 120
ggagcaatcc aacattctct cctgcacgac ctctggggag ttctttttct aacatttcaa 180
ccccagtaac aatcgtttct tttagtatct taagacgac caactgaact ttatcgga 240
ctttaacaat tccacgtcca atacgtccag ttactacagt tctctgtccg gagatagaga 300
acacgtctct aatgggcatt aag 323

```

```

<210> 71
<211> 715

```

<212> DNA

<213> Chlamydia

<400> 71

```

gatccgaatt  cggcagcagag  aaaaaaagat  tctctaacca  ttataaatatc  tgtgatttat  60
gaccocatcaa  cataaaaaaa  tcagcgaaga  aacaatcgcc  tgtgacatgc  tagagcggct  120
ataccggcttc  taccattcaa  gaggttccagc  cctatctcct  tcttactaat  ttgggtatt  180
acgtggatgt  ttctcgctgaa  atctatcagg  tccctgtttc  tcgaggatcc  atgttttcgg  240
gcagcgcatg  cgccctcaat  tcacacctca  atcatcgatt  ttaaattagg  ctctccagga  300
gcagctcttta  ccgtagatct  gtgttctttc  ctcccaatg  ctacagcagc  gatcatgttg  360
ggcatgtgctg  gaggcttaag  atcccactac  caaataggag  attattttgt  cctctgttgc  420
agcatccgaa  aagatggaac  atcagatgca  tacttcccc  cagaggtccc  tgcattagct  480
aattttgtcg  tacaaaaaat  gatcaccaat  attctcgaa  ccaaaaaact  cctctaccat  540
ataggcatca  cccacacgac  taacattcgg  ttttgggagt  ttaataaaga  gtccgctoga  600
aaactatatg  aaaataaagc  tcaaacctgc  gagatggagt  gtgccacctt  atttctgtca  660
ggataccgaa  ggaattcttc  tttaggagca  cttttgctga  tatcggtatc  acctt  715

```

<210> 72

<211> 641

<212> DNA

<213> Chlamydia

<220>

<221> unsure

<222> (550)

<223> n=A,T,C or G

<221> unsure

<222> (559)

<223> n=A,T,C or G

<221> unsure

<222> (575)

<223> n=A,T,C or G

<221> unsure

<222> (583)

<223> n=A,T,C or G

<221> unsure

<222> (634)

<223> n=A,T,C or G

<221> unsure

<222> (638)

<223> n=A,T,C or G

<400> 72

```

gatccgaatt  cggcagcaga  tctcctcgag  ctogatcaaa  cccacacttg  ggacaagtac  60
ctacaacata  acggtccgct  aaaaacttcc  ctctctcttc  agaatacagc  tgttcgggtca  120
cctgattctc  taccagtcgc  cgttctcgca  agtttcgata  gaaatcttgc  acaatagcag  180
gatgataagc  gttcgtagtt  ctggaaaaga  aatctacaga  aattcccaat  ttcttgaagg  240
tatctttatg  aagcttatga  tacatgtcga  cataattctg  ataccccaat  cctgcacaact  300
ctgcattaa  ggtaattgag  attccgtatt  catcagaacc  aaaaatatac  aaaacctctt  360
tgcctttag  tctctgaaaa  cgcgcataaa  catctgcagg  caaataagca  cgggtaatat  420
gtccaaaatg  caaaggacca  tttgcgtaag  gcaacgcaga  agtaataaga  atacgggaag  480
attccactat  ttccactgcg  tccagttgta  cagagaagga  tcttttcttc  tggatgttcc  540
gaaaccttgn  tctcttcgnc  tctctctgt  agcanacaa  tgnctctctc  gacatctctt  600
tcagcgtatt  cggactgatg  ccctaaagat  cccnggagnt  t  641

```

<210> 73

<211> 584

<212> DNA

<213> Chlamydia

<220>

<221> unsure

<222> (460)

<223> n=A,T,C or G

<221> unsure

<222> (523)

<223> n=A,T,C or G

<221> unsure

<222> (541)

<223> n=A,T,C or G

<221> unsure

<222> (546)

<223> n=A,T,C or G

<400> 73

```

gaattcggca cgagacattt ctagaatgga accggcaaca aacaaaaact ttgtatctga 60
agatgacttt aagcaatctt tagataggga agattttttg gaatgggtct ttttatttgg 120
gacttattac ggaacgagta aggcggagat ttctagagtt ctgcacaaagg gtaagcactg 180
catagccgtg attgatgtac aaggagcttt ggctctgaag aagcaaatgc cggcagtcac 240
tatttttatt caagctccct ctcaagaaga acttgagcgc cgtttgaatg ctccggattc 300
agagaagaat ttccagaaga aagaagaatt agagcatagc gctgtcgaaa ttgctgccgc 360
tagcgaattt gattatgttg tggtaaatga tgatttgatt acagcatatc aagttttaag 420
aagtattttt atagctgaag aacataggat gagtcatggn tagaaaaagt cgtttaacta 480
atgaagactc gaataagcta ttgatagacc ctttttagtt ggntaattac gtaatttaag 540
nagctnagaa caaaattgct agaggagatg ttctgttctc taac 584

```

<210> 74

<211> 465

<212> DNA

<213> Chlamydia

<400> 74

```

gatccgaatt cggcagcagc tcgtgccgtt tgggatcgtg taatcgcac ggagaattgt 60
taagaaatta ttttcgagtg aaagagctag gcgtaatcat tacagatagc catactactc 120
caatcgccgc tggagtactg ggtatcgccc tgtgttggtg tggattttct ccattacaca 180
actatatagg atcgctagat tgtttcggtc gtcccttaca gatgacgcga agtaactctg 240
tagatgcctt agcagtttgc gctgtgtttt gtatgggaga ggggaatgag caaacaccgt 300
tagcgggtgat agagcaggca cctaatatgg tctaccatc atactctact tctcagaagg 360
agtattgttc tttgcgata gatgaaacag aggcattata cggacctttt ttgcaagcgg 420
ttaccgtgga gtcaagaaaa gaaatgatgg aggtgtttat gaatt 465

```

<210> 75

<211> 545

<212> DNA

<213> Chlamydia

<400> 75

```

gaattcggca cgagatgaaa agtttagctc acaggggatt ctctaccac agaattccga 60
aaagttttct tccaaaaacc tcttctctctc ttgattagtg atccctctgc aactacttta 120
ctatatgttc tgtgaaatat gcatagtctt caggatttga aatcccaaag tactcagcta 180
atccacgaat tttctctcta gcgatacgtg gaattttgact ctcataagaa tacaaagcag 240
ccactcctgc agctaaagaa tctcctgtac accaccgcac aagaagttagt actttcgtt 300
ttgctgcttc actaggctca tgagcctcta actcttctg agtaactcct agagcaaaaa 360
caaacgtctt ccacaaatca atatgattag ggtaacgctt ctcttctatc atcaagttaa 420
ctaacaataa cttacgcgcc tctaatcat cgcaacgact atgaatcgca gataaatatt 480
taggaaaagg tttgatattg aaataatagt ctttggcata cgctgtaat tgctctttag 540

```

taagc

545

<210> 76

<211> 797

<212> DNA

<213> Chlamydia

<220>

<221> unsure

<222> (788)

<223> n=A,T,C or G

<221> unsure

<222> (789)

<223> n=A,T,C or G

<400> 76

```

gatccgaatt  cggcgcgaga  tacgctagat  gcgataaatg  cggataatga  ggattatcct  60
aaaccagggtg  atttcccacg  atcttctctt  tctagtacgc  ctctctatgc  tccagtagct  120
caatctcgaga  ttccaaacgtc  acctacctca  acacagcctc  catcaccccta  acttgtaaaa  180
actgtaataa  aaagagcgcg  cttctctttt  gcaaaatcaa  ttgtgaacaac  tcttactaga  240
attagggaact  caaatcaaca  gccctcttac  tcttgattcc  aataatgcct  gtatagtctg  300
ctttggatgc  aacaatgttg  ctgtacaaat  tgaagaggat  ggtaattcag  gattttttagt  360
tgctggagctc  atgcttggaa  aacttccaga  gaataccttt  agacaaaaaa  ttttcaaacg  420
tgctttgtct  atcaatggat  ctccgcaatc  taatattaaa  ggcaactctag  gatacgggtg  480
aatctctaac  caactctatc  tctgtgatcg  gcttaacatg  acctatctaa  atggagaaaa  540
gctgcgccgt  tacttagttc  ttttttcgca  gcatgccaat  atctggatgc  aatctatctc  600
aaaaaggagaa  ctccagatt  tacatgctct  aggtatgtat  cacctgtaaa  ttatgcgcgt  660
attatcccaa  tcccgagcta  tcatccagca  atcttccatt  cgaagatttt  ggaatcagat  720
agatacttct  ctaagcatg  ggggtatgct  taccggttat  ttttctcttc  atactcaaaa  780
aaagtgtgng  gggaata  797

```

<210> 77

<211> 399

<212> DNA

<213> Chlamydia

<400> 77

```

catatgcac  accatcacca  tcacatgcga  cgcacatggt  gaattgatat  tcttgcaaac  60
aaaaagttaa  aatatagttc  gacatatatt  tatggaatag  gatcagctcg  ttctgatgaa  120
atcatataaa  agttgaagtt  agatcctgag  gcaagagcct  ctgaattaac  tgaagaagaa  180
gtaggacgac  tgaactctct  gctacaatca  gaatataccg  tagaagggga  ttgacgagt  240
cgtgttcaat  cggatatcaa  aagattgac  gccatccatt  ctatcagagg  tcagagacat  300
agactttctt  taccagtaag  aggacaacgt  acaaaaacta  attctcgtag  tcgaaaaggt  360
aaaagaaaaa  cagtcgcagg  taagaagaaa  taagaatttc  399

```

<210> 78

<211> 285

<212> DNA

<213> Chlamydia

<400> 78

```

atgcacacc  atccaccatca  catgagtcaa  aaaaaataaa  actctgcttt  tatgcatccc  60
gtgaatat  ccacagattt  agcagttata  gttggcaagg  gacctatgcc  cagaaccgaa  120
attgtaaga  aagttttgga  atacattaaa  aaacacaaact  gtcaggatca  aaaaaataaa  180
cgtaatatcc  ttcccgatgc  gaatcttgcc  aaagtctttg  gctctagtga  tccatcgac  240
atgttccaaa  tgaccaaacg  cctttccaaa  catattgtaa  aataa  285

```

<210> 79

<211> 950

<212> DNA

<213> Chlamydia

<400> 79

```

aaattaaactc gagcacaat  tacggcaatt  gctgagcaaa  agatgaagga  catggatgctc  60
gttccttttag agtccgcga  gagaatggtt  gaagggaactg  cccgaagcat  ggggttagat  120
gtagacttaag tagttaaaga  gctgcataat  tatgacaaag  catggaaaac  gcattcgttg  180
tatccaagag  acttacgatt  tagctaagtc  gtattctttg  ggtgaagcga  tagatatttt  240
aaaacagtgt  cctactgtgc  gtttcgatca  aacggttgat  gtgtctgtta  aattagggat  300
cgatccaaga  aagagtgtac  agcaaatcgc  tgggttcggtt  tctttaccctc  acggtacagg  360
taaagttttg  cgaattttag  tttttgctgc  tggagataag  gctgcagagg  ctattgaagc  420
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cttcgatgtt  gcggttgcca  ctcccgatat  gatgagagag  gtcggaaagc  taggaaaagt  540
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taaaaactatt  gcggaaactgc  gaaaaggtaa  aattgaattt  aaagctgatac  gagctgtgtg  660
atgcaacgtc  ggagtgtcga  agctttcttt  cgatagtgcg  caaatcaag  aaaaattgtga  720
agcgttgtgt  gcagccttag  ttaaagctaa  gccgcgaact  gctaaaggac  aatatattag  780
taattcact  atttctcga  ccatggggcc  aggggttacc  gtggatacta  gggagttgat  840
tcgcttataa  ttctaatgtt  aaagaggaaa  aatgaagaa  gagaaaaagt  tgctgcttcg  900
cgaggttgaa  gaaaagataa  ccgcttctca  aggttttatt  ttgttgagat  950

```

<210> 80

<211> 395

<212> DNA

<213> Chlamydia

<400> 80

```

tttcaaggat  tttgttttcc  cgatcatett  actaaatgca  gctccaacaa  tcacatcatg  60
ggctggttta  gcatctaagg  caacagaagc  tcctctgctg  taataagtg  attcttcaga  120
agtaggtgtt  cctactctgc  atagcatcgt  tcctagtcct  gatataccca  ggttggtata  180
gctaactcca  tcaaacgcga  ctgattcat  tttatcgttg  agcaagcctt  gtttgactgt  240
gaccattgac  atttgagatc  ccagaatcga  gttcgcatag  aaatgatgt  ctctaggtac  300
ataagcccat  tgtctataag  agtcaaat  ccagagcgct  gagatcgctt  cattttgtag  360
ttgatcagga  tccagagtga  gtgttctcgt  atatc  395

```

<210> 81

<211> 2085

<212> DNA

<213> Chlamydia

<400> 81

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atttggcgaa  ggagtgtggg  ctacggtcat  taataaatca  ttcgtgttgc  ctgcctccaa  60
gaccagattg  tgtactttct  tatgaagaat  ctctatttga  gcaaatgttg  cgttggggag  120
agctccagtt  agaacaattt  gctcaagtag  gtttagatag  aagttggcaa  gttgttttgc  180
atccaggaat  aggtattggg  aagactccgc  ttcagtogat  gtatttgatg  gatggagtaa  240
agcagtttaa  acgtgtttta  gagtgtcctg  tatataaggg  ccattctaga  aaactcgtgt  300
tgagtattgt  gggccgattt  aatagtgacg  atcgtgattg  ggaacagatc  ggctgttctg  360
tatctcttca  tgcagagga  gttgattatc  tacgtgtgca  tcaggttgaa  ggtaacagac  420
gtgccttagc  cgtctgtcgt  tgggctggta  tgtttgtatg  atccaaagca  aggttatcgt  480
tgctattgat  cccagaggag  tgatgggagc  tttaggcaag  ctcccttgga  gttatccgga  540
agatctacgt  ttttttcag  aaaccattcg  aaatcatccc  atcattatg  agcagaagac  600
ttgggagtc  ctctccagaca  agtataagca  tggggcggat  atcgttgtct  tttctcgcag  660
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tcgaaaagct  tggttttgca  cacatatcaa  aaagaaatat  tggggcgata  ctcttctccc  840
tatcacgcga  ttatcaggat  ggaagaagga  atgtatttgt  aatcacagag  atttcagtat  900
ttattattat  gaaaataact  ccgatcaaaa  caggtaaagt  atttgcacat  gattcgcttc  960

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<210> 82
 <211> 405
 <212> DNA
 <213> Chlamydia

```

<400> 82
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ttctccctgt cttatgggct gttatatggc agtcggaggg tttttccgc gcttatattt 180
cttcggtgac tgatggggat ggttaagagc atttctaaga atttctaat 240
atagtgtgca ggacatggaa gatcttgatc ctccaggacc gccctccttg gaagaattgt 300
attggctcca taaagggagg agaaaacttc gatalagggg atcgatatca ggtgaagata 360
gcaaaaaata aattagctcc tccattccga actgcagaat ttgat 405

```

<210> 83
 <211> 379
 <212> DNA
 <213> Chlamydia

```

<400> 83
tataccattc gtttgaaagt gcctttgacg ggagaaagtg tttttgaaga tcaatgcaa 60
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ttccctacgt atccatttgc taatgtagtt gatgatcatt tgatggggat taccctatgt 180
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gggtggggag ctccgcagtt ttcccatatg ccgcttcttc taatcctga tgggaagtaag 300
ctttccaaga gaaagaatcc tacttctatt ttttactatc gggatgctgg atacaaaaaa 360
gaagcggtca tgaatttcc 379

```

<210> 84
 <211> 715
 <212> DNA
 <213> Chlamydia

```

<400> 84
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cgcttccat tcttgatgca ataatatctg ctgagactaa gaacatgctc ccagagcttt 180
tgggtgtgac tgtgaatttt cctatttcag ttctcctcaa taaagtttca atgttctcgg 240

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```

gagtgataaa cccgttgcat tgaattttat tagtgattgg aaagtgtgta aaagctttca 300
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caatagtatc agcaattcca ccaagaattt gatctcccaa cttttctaga ataagctgggt 420
aagctttttc cgcattccaa ccaattgttaa tagaagcatt ggttgatgga ttattggaga 480
ctgttaaga tatccatca gaagctgtca ttttggctgc gacaggtgtt gatgtgtgtc 540
caaggtattt ttgtgtgtcc ttgagcggct ctgtcatttg cccaactttg atattatcag 600
caaaagcgca gttttgagtg ttatataaat aaaaaccaga atttccattt ttaaaactct 660
tttttatatt gagctttaaa taaattaggt ttttagtttc aaagtgtgta ttaat 715

```

<210> 85
 <211> 476
 <212> DNA
 <213> Chlamydia

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<400> 85
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taggacaaat ggagtaccag ggaggaggag ctctatttgg tgaataatatt tctctttctg 420
agaatgctgg tgtgctcacc tttaaagaca acattgtgaa gacttttgct tcgaat 476

```

<210> 86
 <211> 1551
 <212> DNA
 <213> Chlamydia

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<400> 86
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```

<210> 87

<211> 3031

<212> DNA

<213> Chlamydia

<400> 87

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<210> 88

<211> 976

<212> DNA

<213> Chlamydia

<400> 88

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agggtggatgg ggcgcctgtc caagatgtgc tcgctactct atatggaagc aatcacaaag 60
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```

<210> 89

<211> 94

<212> PRT

<213> Chlamydia

<400> 89

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Met His His His His His His Met Ser Gln Lys Asn Lys Asn Ser Ala
      5                      10                      15

Phe Met His Pro Val Asn Ile Ser Thr Asp Leu Ala Val Ile Val Gly
      20                      25                      30

Lys Gly Pro Met Pro Arg Thr Glu Ile Val Lys Lys Val Trp Glu Tyr
      35                      40                      45

Ile Lys Lys His Asn Cys Gln Asp Gln Lys Asn Lys Arg Asn Ile Leu
      50                      55                      60

Pro Asp Ala Asn Leu Ala Lys Val Phe Gly Ser Ser Asp Pro Ile Asp
      65                      70                      75                      80

Met Phe Gln Met Thr Lys Ala Leu Ser Lys His Ile Val Lys
      85                      90

```

<210> 90

<211> 474

<212> PRT

<213> Chlamydia

<400> 90

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Met Ala Ser His His His His His Met Asn Glu Ala Phe Asp Cys
      5                      10                      15

Val Val Ile Gly Ala Gly Pro Gly Gly Tyr Val Ala Ala Ile Thr Ala

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20	25	30
Ala Gln Ala Gly Leu Lys Thr	Ala Leu Ile Glu Lys Arg	Glu Ala Gly
35	40	45
Gly Thr Cys Leu Asn Arg Gly Cys Ile Pro Ser Lys Ala Leu Leu Ala		
50	55	60
Gly Ala Glu Val Val Thr Gln Ile Arg His Ala Asp Gln Phe Gly Ile		
65	70	75
His Val Glu Gly Phe Ser Ile Asn Tyr Pro Ala Met Val Gln Arg Lys		
85	90	95
Asp Ser Val Val Arg Ser Ile Arg Asp Gly Leu Asn Gly Leu Ile Arg		
100	105	110
Ser Asn Lys Ile Thr Val Phe Ser Gly Arg Gly Ser Leu Ile Ser Ser		
115	120	125
Thr Glu Val Lys Ile Leu Gly Glu Asn Pro Ser Val Ile Lys Ala His		
130	135	140
Ser Ile Ile Leu Ala Thr Gly Ser Glu Pro Arg Ala Phe Pro Gly Ile		
145	150	155
Pro Phe Ser Ala Glu Ser Pro Arg Ile Leu Cys Ser Thr Gly Val Leu		
165	170	175
Asn Leu Lys Glu Ile Pro Gln Lys Met Ala Ile Ile Gly Gly Gly Val		
180	185	190
Ile Gly Cys Glu Phe Ala Ser Leu Phe His Thr Leu Gly Ser Glu Val		
195	200	205
Ser Val Ile Glu Ala Ser Ser Gln Ile Leu Ala Leu Asn Asn Pro Asp		
210	215	220
Ile Ser Lys Thr Met Phe Asp Lys Phe Thr Arg Gln Gly Leu Arg Phe		
225	230	235
Val Leu Glu Ala Ser Val Ser Asn Ile Glu Asp Ile Gly Asp Arg Val		
245	250	255
Arg Leu Thr Ile Asn Gly Asn Val Glu Glu Tyr Asp Tyr Val Leu Val		
260	265	270
Ser Ile Gly Arg Arg Leu Asn Thr Glu Asn Ile Gly Leu Asp Lys Ala		
275	280	285
Gly Val Ile Cys Asp Glu Arg Gly Val Ile Pro Thr Asp Ala Thr Met		
290	295	300
Arg Thr Asn Val Pro Asn Ile Tyr Ala Ile Gly Asp Ile Thr Gly Lys		
305	310	315
Trp Gln Leu Ala His Val Ala Ser His Gln Gly Ile Ile Ala Ala Arg		
325	330	335


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Asn Ile Gly Gly His Lys Glu Glu Ile Asp Tyr Ser Ala Val Pro Ser
      340                      345                      350

Val Ile Phe Thr Phe Pro Glu Val Ala Ser Val Gly Leu Ser Pro Thr
      355                      360                      365

Ala Ala Gln Gln Gln Lys Ile Pro Val Lys Val Thr Lys Phe Pro Phe
      370                      375                      380

Arg Ala Ile Gly Lys Ala Val Ala Met Gly Glu Ala Asp Gly Phe Ala
      385                      390                      395                      400

Ala Ile Ile Ser His Glu Thr Thr Gln Gln Ile Leu Gly Ala Tyr Val
      405                      410                      415

Ile Gly Pro His Ala Ser Ser Leu Ile Ser Glu Ile Thr Leu Ala Val
      420                      425                      430

Arg Asn Glu Leu Thr Leu Pro Cys Ile Tyr Glu Thr Ile His Ala His
      435                      440                      445

Pro Thr Leu Ala Glu Val Trp Ala Glu Ser Ala Leu Leu Ala Val Asp
      450                      455                      460

Thr Pro Leu His Met Pro Pro Ala Lys Lys
      465                      470

<210> 91
<211> 129
<212> PRT
<213> Chlamydia

<400> 91
Met His His His His His Met Pro Arg Ile Ile Gly Ile Asp Ile
      5                      10                      15

Pro Ala Lys Lys Lys Leu Lys Ile Ser Leu Thr Tyr Ile Tyr Gly Ile
      20                      25                      30

Gly Ser Ala Arg Ser Asp Glu Ile Ile Lys Lys Leu Lys Leu Asp Pro
      35                      40                      45

Glu Ala Arg Ala Ser Glu Leu Thr Glu Glu Glu Val Gly Arg Leu Asn
      50                      55                      60

Ser Leu Leu Gln Ser Glu Tyr Thr Val Glu Gly Asp Leu Arg Arg Arg
      65                      70                      75                      80

Val Gln Ser Asp Ile Lys Arg Leu Ile Ala Ile His Ser Tyr Arg Gly
      85                      90                      95

Gln Arg His Arg Leu Ser Leu Pro Val Arg Gly Gln Arg Thr Lys Thr
      100                     105                     110

Asn Ser Arg Thr Arg Lys Gly Lys Arg Lys Thr Val Ala Gly Lys Lys
      115                     120                     125

```

Lys

<210> 92

<211> 202

<212> PRT

<213> Chlamydia

<400> 92

Met His His His His His His Met Gly Ser Leu Val Gly Arg Gln Ala
5 10 15

Pro Asp Phe Ser Gly Lys Ala Val Val Cys Gly Glu Glu Lys Glu Ile
20 25 30

Ser Leu Ala Asp Phe Arg Gly Lys Tyr Val Val Leu Phe Phe Tyr Pro
35 40 45

Lys Asp Phe Thr Tyr Val Cys Pro Thr Glu Leu His Ala Phe Gln Asp
50 55 60

Arg Leu Val Asp Phe Glu Glu His Gly Ala Val Val Leu Gly Cys Ser
65 70 75 80

Val Asp Asp Ile Glu Thr His Ser Arg Trp Leu Thr Val Ala Arg Asp
85 90 95

Ala Gly Gly Ile Glu Gly Thr Glu Tyr Pro Leu Leu Ala Asp Pro Ser
100 105 110

Phe Lys Ile Ser Glu Ala Phe Gly Val Leu Asn Pro Glu Gly Ser Leu
115 120 125

Ala Leu Arg Ala Thr Phe Leu Ile Asp Lys His Gly Val Ile Arg His
130 135 140

Ala Val Ile Asn Asp Leu Pro Leu Gly Arg Ser Ile Asp Glu Glu Leu
145 150 155 160

Arg Ile Leu Asp Ser Leu Ile Phe Phe Glu Asn His Gly Met Val Cys
165 170 175

Pro Ala Asn Trp Arg Ser Gly Glu Arg Gly Met Val Pro Ser Glu Glu
180 185 190

Gly Leu Lys Glu Tyr Phe Gln Thr Met Asp
195 200

<210> 93

<211> 19

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> made in a lab

<400> 93

Glu Asn Ser Leu Gln Asp Pro Thr Asn Lys Arg Asn Ile Asn Pro Asp
1 5 10 15
Asp Lys Leu

<210> 94

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 94

Asp Pro Thr Asn Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys
1 5 10 15
Val Phe Gly Thr
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<210> 95

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 95

Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys Val Phe Gly Thr
1 5 10 15
Glu Lys Pro Ile
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<210> 96

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 96

Asp Asp Lys Leu Ala Lys Val Phe Gly Thr Glu Lys Pro Ile Asp Met
1 5 10 15
Phe Gln Met Thr
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<210> 97

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 97
Lys Val Phe Gly Thr Glu Lys Pro Ile Asp Met Phe Gln Met Thr Lys
1 5 10 15
Met Val Ser Gln
20

<210> 98
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 98
Asn Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys Val Phe Gly
1 5 10 15
Thr Glu Lys Pro
20

<210> 99
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 99
Asn Lys Arg Asn Ile Leu Pro Asp Ala Asn Leu Ala Lys Val Phe Gly
1 5 10 15

<210> 100
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 100
Lys Met Trp Asp Tyr Ile Lys Glu Asn Ser Leu Gln Asp Pro Thr
1 5 10 15

<210> 101
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 101
Thr Glu Ile Val Lys Lys Val Trp Glu Tyr Ile Lys Lys His Asn Cys
1 5 10 15
Gln Asp Gln Lys
20

<210> 102
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 102
 Lys Val Trp Glu Tyr Ile Lys Lys His Asn Cys Gln Asp Gln Lys Asn
 1 5 10 15
 Lys Arg Asn Ile
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<210> 103
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 103
 Lys Val Trp Glu Tyr Ile Lys Lys His Asn Cys Gln Asp Gln Lys
 1 5 10 15

<210> 104
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 104
 Ala Glu Leu Thr Glu Glu Glu Val Gly Arg Leu Asn Ala Leu Leu Gln
 1 5 10 15
 Ser Asp Tyr Val
 20

<210> 105
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 105
 Leu Gln Ser Asp Tyr Val Val Glu Gly Asp Leu Arg Arg Arg Val Gln
 1 5 10 15
 Ser Asp Ile Lys Arg
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<210> 106
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
<223> Made in a lab

<400> 106
Met Pro Arg Ile Ile Gly Ile Asp Ile Pro Ala Lys Lys Lys Leu Lys
1 5 10 15
Ile Ser Leu Thr
20

<210> 107
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 107
Ala Glu Leu Thr Glu Glu Glu Val Gly Arg Leu Asn Ala Leu Leu Gln
1 5 10 15
Ser Asp Tyr Val
20

<210> 108
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 108
Leu Asn Ala Leu Leu Gln Ser Asp Tyr Val Val Glu Gly Asp Leu Arg
1 5 10 15
Arg Arg Val Gln
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<210> 109
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 109
Leu Asn Ser Leu Leu Gln Ser Glu Tyr Thr Val Glu Gly Asp Leu Arg
1 5 10 15
Arg Arg Val Gln
20

<210> 110
<211> 1461
<212> DNA
<213> Chlamydia

<400> 110

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tgctagaag cccatatccct actccacett tgctctctag atatcagcta cagaatatgg 180
atgtagaagc agggttccgt gaggcagttt atgcttcttt tgtagcagga atgtacaatt 240
atgtagttag acagcccgaa gagcgatttc ccaatagtca gcaggttgaa gggattctgc 300
gtgatattgt taccacacggg tcacagacat tttagcaacct gatgcagcgt tgggatatag 360
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gctccattga ggaggatgct aaacaagaaa ttcgctatca gacagaaagg tttaaacagc 660
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taaagactcc tcagatattg catctgagag ttagggggttc cttttgctta cggcgcttta 840
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ggacagatta gagaaaaatg agcaagcttt attgtccgat gtgcgcttag ttttatctag 1440
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<210> 111

<211> 267

<212> DNA

<213> Chlamydia

<400> 111

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acagaattcg tggaggattc cgggttttgcg cagttaaagc tccaggtctt ggagatagaa 120
gaaaagctat gtttgaagac atcgcttatct taactggcgg tcaactcatt agcgaagagt 180
tgggcatgaa attagaaaac gctaacttag ctatgttagg taaagctaaa aaagtatatc 240
tttctaagaa agacacgacc atcgctg

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<210> 112

<211> 698

<212> DNA

<213> Chlamydia

<400> 112

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tgaaaattcc tacgagaagg agctggcatg cttagaaaag aaacgcagta gcgtacaaaa 120
agatctgagc caactgaaaa aatacacagt tctctacatc aagaagctgc tcgaaacctt 180
cagacaaactc gggcatcgaa agacaaaaat tgcaaaattt gatgcacctc ctaccgagag 240
agtctccgct cataaagaag caaaagaact cgtcgcgctc gatcaagaag agaaactcta 300
aaacgtgact cggcccttga gatccttaaa ctctcgggcc aaaaagacta cagtctcttc 360
gagaagaaaa acggtgttag aaaatacgcg cgctaagact tctctcaaca atgactcaaa 420
aagctgtaaa cgtatacgtt tacgcgtctt ccataatttc taggctgatt tccacattat 480
ctcgacttgc tacggaaaac aataaagtac ggatagcctt aatagtgcgt cctctcttca 540
cgataatttt acogatactc cctctagcaa cagtcgaatt ctgataatc gtattgggtc 600
cctgcacctc tttcagatgc acttctctcg gcttataaac aagatttttt acaatgtacg 660
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```

<210> 113

<211> 1142

<212> DNA

<213> Chlamydia

<400> 113

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ctcttcaaaag attgtgaggt tatgtgaagg cgtgtgcgt gatgcaagaa tgtgcaaacg 60
agagttgata aaaaaagaag cggatgctta ttgttttgt gagaaaaagc ggataatatct 120
aacgcaaaaaa gaaggtatatt tgattccctc tgcaggaggt gatgaatcga atcaggacca 180
gccttttgtt ttatatccta aagatatttt gggatcgtgt aatgcgatcg gagaatgggt 240
aagaaattat ttctgagtga aagagctagg cgtaatcatt acagatagcc atactactcc 300
aatggcgctg ggagttactgg gtatcgggct gtgttggtat ggattttctc cattacacaa 360
ctatatagga tcgctagatt gtttcggctg tcccttacag atgacgcaaa gtaactctgt 420
agatgcctta gcagttgcgg ctgttgtttg tatgggagag ggaatgagc aaacaccggt 480
agcgggtgata gagcaggcac ctaatatggt ctaccattca taccctact ctogagaaga 540
gtattgttct ttgcgcatag atgaaacaga ggactttatc ggaccttttt tgcaagcggt 600
tacgtggagt caagaaaaaga aatgatggag gtgtttatga attttttaga tcagttagat 660
ttaattattc aaaaataagca tatgctagaa cacacgtttt atgtgaaatg gtogaaaggg 720
gagcttacta aagagcaatt acaggcggtat gccaaagact attatttaca tatcaagacc 780
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ggagtggtcg ctttgtattc ttatgagagt caaattccac gtatcgctag agagaaaatt 1080
cgtggattga ctgagtactt tggattttcc aatcctgaag actatgcata tttcacagaa 1140
ca

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1142

<210> 114

<211> 976

<212> DNA

<213> Chlamydia

<400> 114

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ggactgcagc tgaagagtgc gctgctttaa gaacactatt ttctcgcagc gcctcttttag 120
ggcacaaagt acctctctgg cgcaactactt taaagattcg tcgtcctttt ggtactacga 180
gagaagttcg tgtgaaatgg cgttatgttc ctgaaggtgt aggagatttg gctaccatag 240
ctctctctat cagggtccca cagttacaga aatcgatgag aagctttttc cctaagaaaag 300
atgatcggtt tcactggtct agttcgctat tctactctcc aatggttccg catttttggg 360
cagagcttcg caatcattat gcaacgagtg gtttgaaaag cgggtacaaat attgggagta 420
ccgatgggtt ttccctctgc attgggctg ttatatggga gtccgagggt cttttccgcg 480
cttatatttc ttctggtact gatggggatg gtaagagcca taaagttaga tttctaagaa 540
ttctacataa tagttggcag gacatggaag attttgatcc ttacaggacg cctccttggg 600
aagaatttgc taagattatt caagtatttt ctctcaatac agaagctttg attatcgacc 660
aacgacaacaa cccaggtggt agtgctcttt atctttatgc actgctttcc atgttgacag 720
accgtccttt agaacttctc aaacatagaa tgattctgac tcaggatgaa gtgttgatg 780
ctttagattg gttaaccctg ttggaaaacg tagacacaaa cgtggaggtc cgccttgctc 840
tgggagacaa catggaagga tatactgtgg atctacaggt tgccgagtat taaaaagct 900
ttggacgtca agtatgtaat tgttggagta aaggggatat cgagttatca acacctattc 960
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976

<210> 115

<211> 995

<212> DNA

<213> Chlamydia

<400> 115

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ttatcttaga aatttgggtg tcaatatgag cgaaaaaaga aagtctaaca aaattattgg 60
tatcgacctc gggacgacca actcttgcgt ctctgttatg gaagtggtcc aacctaaagt 120

```



```

tattgctctct tctgaaggaa ctctgtactac tctctctatc gttgctttta aagggtggcga 180
aactcttgtt ggaattcctg caaaacgtca ggcagtaacc aatcctgaaa aaacattggc 240
ttctactaag cgattcatcg gttagaaaatt ctctgaagtc gaatctgaaa ttaaacacagt 300
ccctctacaaa gttgtctccta actcgaaagc agatgcggtc tttgatgtgg acaaaaaact 360
gtacactcca gaagaaatcg gcgctcagat cctcatgaag atgaaggaaa ctgctgagcg 420
ttatctcgga gaacagtaaa cgggaagcagt cttaccgcta ccagcttact ttaacgattc 480
tcaaaagagct tctacaaaag atgtcggacg tatcgcagga ttagatgtta aacgcattat 540
tctgaacca acagcgggccc ctcttgctta tggattgat aaggaaaggag ataaaaaaat 600
cgccgtcttc gacttaggag gaggaacttt cgatatttct atcttgaaaa tcgggtgacg 660
agtttttgaa gttctctcaa ccaacgggga tactcacttg ggaggagacg actctgacg 720
agtcctcttc aactggatgc ttgatgaatt caaaaaacaa gaaggcattg atctaagcaa 780
agataacatg gctttgcaaa gattgaaaga tgctgctgaa aaagcaaaaa tagaattgtc 840
tggtgtatcg tctactgaaa tcaatcagcc attcatcact atcgacgcta atggacctaa 900
acatttgctc ttaactctaa ctgcgcctca attcgaacac ctgacttctc ctctcattga 960
gcgacccaaa caactctgtg ctccagcttt aaaag 995

```

<210> 116

<211> 437

<212> DNA

<213> Chlamydia

<400> 116

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ggaattatcg aaattgcaca taacaaagcg acagatgttg gaggtgtgtc ttacgtaaaa 120
ggaaccttta cttgtgaaaa ctctcaccgt ctacaatttt tgaaaaactc ttccgataaa 180
caagggtggag gaattcagcg agaagacac atcaccctat ctaatttgac aggggaagact 240
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aaagctctta caatgacagg actggaatgt ttctgtttaa ttaataaacac atcagaaaaa 360
catggtgttg gagcctttgt taccaaaaga atctctcaga cttacacctc tgatgtggaa 420
acaattccag gaatcac 437

```

<210> 117

<211> 446

<212> DNA

<213> Chlamydia

<400> 117

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aagtttacct agaccaaaact gaagatgacg aaggaaaaagt tgttttatcc agagaaaaag 60
caacaagaca acgacaatgg gaatacatct ttgtctactg cgaggaaagt tctattgtta 120
agggacaaaat taccgcaaaa gtttaagggtg gtttgatcgt agataattgt atgggaagcct 180
tctctccagg attcccaata gacaataaga agatcaagaa cttagatgat tacgtaggca 240
aggtttgtga gttcaaaaat ctcaaaaatca acgtggaatg tcgggaacgtt gttgttatcta 300
gaagagaact tctcgaaact gaacgcattt ctaagaaagc agagttgtag gagcaaatca 360
ctatcgggtg aogtcgcaaa ggtatcgcta agaatacac agatttcgga gtattctctg 420
atcttgatgg cattgacggc ctactc 446

```

<210> 118

<211> 951

<212> DNA

<213> Chlamydia

<400> 118

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agtattgcga aatattactg tgagaagcaa tgctgagagc ggttctagta aaagtggagg 60
gagagctgtc agaaggatc gctcagggaag cgagacaacg tgtggctgat ttattaggaa 120
gattccctct ttatcctgaa atcgatctgg aaacgctagt ttagtgggag actctatgcc 180
tgaaggggaa tggatgcata agttgcaaga tgtcatagat agaaagtgtg ttgattctcg 240
tcgtattttc ttctccgaac ctgtaacgga gaaaagtgtc gcagaagcca tcaaaaagct 300
ttggtatttg gaactcacca atcctgggca gccaatgtta ttgtcatta atagccctgg 360

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```

agggctctgtt gatctgggtt ttgctgtttg ggaccaaatt aaaatgatct cttctccttt 420
gactcacagtt gttacagggt tagcagcatc tatgggatct gtattgagtt tbggtgctgt 480
tccaggaaga cgttttctga cgctcatgc gcgcattatg attcaccagc ctctctattgg 540
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aaaagcagc attattgatg tgtatgtcga ggcaactgga caatctccag aggtgataga 660
gaaagctatc gatcgagata tgtggatgag tgc aaatgaa gcaatggagt ttggactggt 720
agatgggatt ctctctcttt ttaacgactt gtatagattt tttatattct ggagcaggaa 780
acagtctcat tttggggaga tcgatgcctt ctcttgagga ttgtctgttt ttatgccagg 840
aagagatggt tgatgggttt ttatgtgtag agtctctctga aatagcagat gctaaactca 900
ctgtttttaa tagtgatgga tctatcgctt ctatgtgcgg gaatgggttg c 951

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<210> 119

<211> 953

<212> DNA

<213> Chlamydia

<400> 119

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catcaacacc tbtgcagacc aaaatgacag ctctgtatgg aatatcttta acagtctcca 120
ataatccatc aacaaatgct tctattacaa ttgggttggg tcgggaaaaa gcttaccagc 180
ttattctaga aaagtttggg gatcaaatc ttgggtggaat tgctgatact attgttgata 240
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acattgaaac tttattagga ggaactgaaa taggaaaatt cacagtcaca cccaaagct 420
ctgggagcat gttcttagtc tcagcagata ttattgcatt aagaatggaa ggccgctgtg 480
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caggcgcttc taattattgt agtctaagaa ccagaattat taatacagga ttgactccga 600
caacgctatc attactgtga ggcggtttag aaagcggtgt ggtatgggtt aatgcccttt 660
ctaattggca tgatatatta ggaataacaa atactcttaa tgtatctttt ttggaggtaa 720
tacctcaaac aaacgctttaa acaattttta ttgatttttt ctatagggtt ttatatattg 780
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tttataaaat tgttaaaagt tctgtgtatc ggctcgcgat tccgactcgt ccaacatcaa 900
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<210> 120

<211> 897

<212> DNA

<213> Chlamydia

<220>

<221> misc_feature

<222> (1) ... (897)

<223> n = A, T, C or G

<400> 120

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cttaagcttcg ccaagcttgc tgccgaattg accgcaataa ctcggaaaca cgtggagggc 180
gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggtatgcaga 240
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gcggaagag cagattgcga agcccgctgc gctcgttatt cgagagaaga gtcgtcactc 660
gaattgtcgg gagaggaaaa tgcttgcgag aggagagtcg ctggagagaa agccaagacg 720

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ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttga atgcgttgcc 780
gacgttttca aattgggtgc gtgccttatt acaatgggta ttctgtgcaat tgtggctgcg 840
ggatgtaagt tcactctgc agttattgga ttgtggaact tctgcgccag agcataa 897

```

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<210> 121
<211> 298
<212> PRT
<213> Chlamydia

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<400> 121
Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
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Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn
20 25 30
Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
35 40 45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
50 55 60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
65 70 75 80
Thr Val Leu Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
85 90 95
Val Gln Ser Ala Gln Ser Phe Phe Ser Tyr Met Lys Ala Ala Ser Gln
100 105 110
Lys Pro Gln Glu Gly Asp Glu Gly Leu Val Ala Asp Leu Cys Val Ser
115 120 125
His Lys Arg Arg Ala Ala Ala Val Cys Ser Phe Ile Gly Gly Ile
130 135 140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
145 150 155 160
Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Ile Lys Ala Asn Met
165 170 175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Phe Val
180 185 190
Val Gly Ser Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
195 200 205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Ser Leu Glu Leu Ser Gly
210 215 220
Glu Glu Asn Ala Cys Glu Arg Arg Val Ala Gly Glu Lys Ala Lys Thr
225 230 235 240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
245 250 255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
260 265 270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Val
275 280 285
Ile Gly Leu Trp Thr Phe Cys Ala Arg Ala
290 295

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<210> 122
<211> 897
<212> DNA
<213> Chlamydia

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<400> 122
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gttaaggtcg ccaagctcgc tgccgaattg accgcaaata ttttgaaca agctggaggc 180

```

```

gcgggctctt cgcacacat tacagcttcc caagtgtcca aaggattagg ggatacgaga      240
actgttgtcg ctttagggaa tgcccttaac ggagcgttgc caggaaacagt tcaaagtgcg      300
caaaagcttct tctctcacat gaaagctgct agtcagaaaa cgcaagaagg ggaatgagggg      360
ctcacagcag atcttttgtt gtctcataag cgcagagcgg ctgcggttgt ctgtggcttc      420
atcggaggaa ttacctacct cgcgcattc ggagttatcc gtccgattct gtttgcctaac      480
aaaatgtcgg tgaaccogtt tctttcttcc caaactaaag caaatatggg atctcttgtt      540
agctatatta tggcgggctaa ccatgcagcg tctgtggtgg gtgtgtggag cgtctatcagt      600
gcggaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgttactc      660
gaagtgtcgg gagaggaaaa tgcttgcgag aagagagctg ctggagagaa agccaagacg      720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttggg atggtgtgcc      780
gacgttttca aattggtgcc gctgcctatt acaatgggta ttctgtcgat tgtgtgtgct      840
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<210> 123

<211> 298

<212> PRT

<213> Chlamydia

<400> 123

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Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
1      5      10      15
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20     25     30
Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
35     40     45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
50     55     60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Thr Arg
65     70     75     80
Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
85     90     95
Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
100    105    110
Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
115    120    125
His Lys Arg Arg Ala Ala Ala Val Cys Gly Phe Ile Gly Gly Ile
130    135    140
Thr Tyr Leu Ala Thr Phe Gly Val Ile Arg Pro Ile Leu Phe Val Asn
145    150    155    160
Lys Met Leu Val Asn Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
165    170    175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
180    185    190
Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
195    200    205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Ser Gly
210    215    220
Glu Glu Asn Ala Cys Glu Lys Arg Val Ala Gly Glu Lys Ala Lys Thr
225    230    235    240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
245    250    255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
260    265    270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
275    280    285
Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
290    295

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<210> 124
 <211> 897
 <212> DNA
 <213> Chlamydia

<400> 124
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 acacagcccca acaataaaa ggcaagggtg gtaataaaga cgaagggaat ggataagact 120
 attaaaggttg ccaagctctg tgcgaatttg accgcaataa ttttggaaca agctggaggc 180
 gcgggctctt cgcacacacat tacagcttcc caagtgcca aaggattagg ggaatgcgaga 240
 actgtgtctg ctttagggaa tgcccttaac ggagcgttgc caggaacagt tcaaatgtgc 300
 caaagcttct tctctcacat gaaagctgct agtcagaaaa cgcaagaagg ggaatgagggg 360
 ctacacagcag atctttgtgt gtctcataag cgcagagcgg ctgcggtctgt ctgtagcatc 420
 atcggaggaa ttacctacct cgcacattc ggagctatcc gtccgattct gttgtccaac 480
 agctatatta tggcggctaa ccatgcagcg tctgtggtgg gtgctggact cgctatcagt 540
 aaaatgtctg caaaaccgtt tctttcttcc caaactaaag caaatatggg atcttctgtt 600
 agctatatta tggcggctaa ccatgcagcg tctgtggtgg gtgctggact cgctatcagt 660
 gcggaagagc cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgttactc 720
 gaagtgcggc gagagggaaa tgcttgcgag aagaaagtgc ctggagagaa agccaagacg 780
 ttacgcggca tcaagtatgc actcctcact atgctcgaga agtttttggg atgctgttgc 840
 gacgttttca aattggtgcc gctgcctatt acaatgggta ttcgtgcgat tgtggtcgtc 897
 ggaatgactg tcaactctgc aattattgga ttgtgcactt tctgcgcagc agcataa

<210> 125
 <211> 298
 <212> PRT
 <213> Chlamydia

<400> 125
 Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
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 Lys Ala Phe Phe Thr Gln Pro Asn Asn Lys Met Ala Arg Val Val Asn
 20 25 30
 Lys Thr Lys Gly Met Asp Lys Thr Ile Lys Val Ala Lys Ser Ala Ala
 35 40 45
 Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
 50 55 60
 Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
 65 70 75 80
 Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
 85 90 95
 Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
 100 105 110
 Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
 115 120 125
 His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Ile Ile Gly Gly Ile
 130 135 140
 Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
 145 150 155 160
 Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
 165 170 175
 Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
 180 185 190
 Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
 195 200 205
 Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Pro Gly
 210 215 220
 Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr
 225 230 235 240

Phe	Thr	Arg	Ile	Lys	Tyr	Ala	Leu	Leu	Thr	Met	Leu	Glu	Lys	Phe	Leu
			245					250						255	
Glu	Cys	Val	Ala	Asp	Val	Phe	Lys	Leu	Val	Pro	Leu	Pro	Ile	Thr	Met
			260					265					270		
Gly	Ile	Arg	Ala	Ile	Val	Ala	Ala	Gly	Cys	Thr	Phe	Thr	Ser	Ala	Ile
		275					280					285			
Ile	Gly	Leu	Cys	Thr	Phe	Cys	Ala	Arg	Ala						
	290					295									

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<210> 126
<211> 897
<212> DNA
<213> Chlamydia
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<40> 126									
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ataagtgttt	ccaagctctgc	tgcgcaattg	accgcaaaat	tttggcaaca	agctcgaggc	180			
cgcggtctctt	cgcacacatc	tacagctcttc	taagcttcca	aaggtatagg	ggaatcgaga	240			
cactgttgtcg	ctctttaggaa	tgtctttaac	ggagctgtgc	caggaaacagt	tcaaatgtcg	300			
caacgctctct	tctctcacat	gaagctgtct	agctcaggaa	cgaagaaggc	ggaatgaggc	360			
ctcacacgag	atctttgtgt	gtctctatac	cgcagatcgc	ctgcgctgtc	cttgatgac	420			
atcggagagc	ttacctactc	cgcgcatttc	ggagatcagg	ctgcgattt	gtttgtcaac	480			
aaaatgctgc	caaaaacgct	tcttctcttc	caaaataaag	caaatatggg	atcttctggt	540			
agctataatg	tggcggctac	ccatgcagcg	ctctgttggt	gtgctgaact	cgcatacagt	600			
cgggaaagtc	cagatttgcga	agcccgctgc	ctctgctatt	cgagagaagg	tgcgttactc	660			
gaagtgcggc	gagaggaaaa	tgtctgcgag	aagaaagctg	ctggagagaa	agccaagaagc	720			
tctacgcgca	tcaagtatgc	actctctact	atgtctgcga	agtttttggg	atgcgtctgc	780			
gagcttttca	aattgtgtcc	gctgctattc	acaaatggta	tctgtgcgat	tgtgtctgct	840			
gcgtctacgt	taactctctc	tcttatttga	tctgtcaact	ctctgcacat	acgataa	897			

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<210> 127
<211> 298
<212> PRT
<213> Chlamydia
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<400> 127																
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1				5				10						15		
Lys	Ala	Phe	Phe	Thr	Gln	Pro	Asn	Asn	Lys	Met	Ala	Arg	Val	Val	Asn	
			20					25					30			
Lys	Thr	Lys	Gly	Met	Asp	Lys	Thr	Ile	Lys	Val	Ala	Lys	Ser	Ala	Ala	
		35					40					45				
Glu	Leu	Thr	Ala	Asn	Ile	Leu	Glu	Gln	Ala	Gly	Gly	Ala	Gly	Ser	Ser	
	50					55					60					
Ala	His	Ile	Thr	Ala	Ser	Gln	Val	Ser	Lys	Gly	Leu	Gly	Asp	Ala	Arg	
65					70				75						80	
Thr	Val	Val	Ala	Leu	Gly	Asn	Ala	Phe	Asn	Gly	Ala	Leu	Pro	Gly	Thr	
				85					90				95			
Val	Gln	Ser	Ala	Gln	Ser	Phe	Phe	Ser	His	Met	Lys	Ala	Ala	Ser	Gln	
			100					105					110			
Lys	Thr	Gln	Glu	Gly	Asp	Glu	Gly	Leu	Thr	Ala	Asp	Leu	Cys	Val	Ser	
			115				120					125				
His	Lys	Arg	Arg	Ala	Ala	Ala	Ala	Val	Cys	Ser	Ile	Ile	Gly	Gly	Ile	
	130				135						140					
Thr	Tyr	Leu	Ala	Thr	Phe	Gly	Ala	Ile	Arg	Pro	Ile	Leu	Phe	Val	Asn	
145					150					155					160	
Lys	Met	Leu	Ala	Lys	Pro	Phe	Leu	Ser	Ser	Gln	Thr	Lys	Ala	Asn	Met	

165 170 175
 Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
 180 185 190
 Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
 195 200 205
 Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Pro Gly
 210 215 220
 Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr
 225 230 235 240
 Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
 245 250 255
 Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
 260 265 270
 Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
 275 280 285
 Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
 290 295

<210> 128
 <211> 897
 <212> DNA
 <213> Chlamydia

<400> 128
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 acacagccca gcaataaaa ggcaagggtta gtaataaaga cgaaggggaat ggataagact 120
 gttaaggtcg ccaagctcgc tgccgaattg accgcaataa ttttggaaac agctggagggc 180
 cggggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatacagga 240
 actgttgttcg ctttagggaa tgcccttaac ggagcgttgc caggaaacagt tcaaaagtgcg 300
 caaagcttct tctctcacat gaaagctgct agtcagaaaa cgaagaagg ggatgagggg 360
 ctccacagcag atctttgtgt gtctcataag cgcagagcgg ctgcggtgt ctgtggcttc 420
 atcggaggaa ttacctacct cgcgacattc ggagttatcc gtccgattct gtttgtcaac 480
 aaaaatgtcg tgaacccgtt tctttcttcc caaactaaag caaatatggg atcttctgtt 540
 agctatatta tggcggctaa ccatgcagcg tctgtggtgg gtgctggact cgctatcagt 600
 cgcgaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgttactc 660
 gaagtgtcgg gagaggaaaa tgcttgcgag aagagagtcg ctggagagaa agccaagacg 720
 ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttgga atcgcttgcc 780
 gacgttttca aattggtgcc gctgcctatt acaatgggta ttgctgcgat tgtggctgct 840
 ggatgtacgt tcactctcgc aattattgga ttgtgcactt tctgcgccag agcataa 897

<210> 129
 <211> 298
 <212> PRT
 <213> Chlamydia

<400> 129
 Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
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 Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn
 20 25 30
 Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
 35 40 45
 Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
 50 55 60
 Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Thr Arg
 65 70 75 80
 Thr Thr Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
 85 90 95

Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
 100 105 110
 Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
 115 120 125
 His Lys Arg Arg Ala Ala Ala Val Cys Gly Phe Ile Gly Gly Ile
 130 135 140
 Thr Tyr Leu Ala Thr Phe Gly Val Ile Arg Pro Ile Leu Phe Val Asn
 145 150 155
 Lys Met Leu Val Asn Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
 165 170 175
 Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
 180 185 190
 Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
 195 200 205
 Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Ser Gly
 210 215 220
 Glu Glu Asn Ala Cys Glu Lys Arg Val Ala Gly Glu Lys Ala Lys Thr
 225 230 235
 Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
 245 250 255
 Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
 260 265 270
 Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
 275 280 285
 Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
 290 295

<210> 130

<211> 897

<212> DNA

<213> Chlamydia

<400> 130

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 gttaaagctgc ccaagtctgc tgccgaattg accgcaataa ttttggaaac agctggaggac 180
 cggggctctct ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatgcgaga 240
 actgttctctg ctttaggggaa tgcccttaac ggagcgttgc caggaacagt tcaaatgtcg 300
 caaagcttct tctctacat gaaagctgct agtcagaaac cgcaagaagg ggaatgagggg 360
 ctctagcagc atcttttgtt gtctcataag cgcagagcgg ctgcggctgt ctgtagcttc 420
 atcggaggaa ttacctacct cgcacattc ggagctatcc gtccgattct gttgtcaac 480
 aaaatgctgg cgcaacgctt tctttcttcc caaactaaag caaatatggg atcttctgtt 540
 agctatatta tggcggctaa ccatgcagcg tttgtgggtg gttctggact cgctatcagt 600
 cgcgaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgtcactc 660
 gaattgtcgg gagaggaaaa tgcttgcgag aggggagtcg ctggagagaa agccaagacg 720
 ttcacgcgca tcaagtatgc actctcact atgctcgaga agtttttgga atgcgttgcc 780
 gacgttttca aattggtgcc gttgctatt acaatgggta ttcgtgcaat tgtggctgcg 840
 ggaatgacgt tcaactctgc agttattgga ttgtggactt tctgcaacag agtataa 897

<210> 131

<211> 298

<212> PRT

<213> Chlamydia

<400> 131

Met Ala Ala Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
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 Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn

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Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala	35	40	45		
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser	50	55	60		
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg	65	70	75	80	
Thr Val Leu Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr	85	90	95		
Val Gln Ser Ala Gln Ser Phe Phe Ser Tyr Met Lys Ala Ala Ser Gln	100	105	110		
Lys Pro Gln Glu Gly Asp Glu Gly Leu Val Ala Asp Leu Cys Val Ser	115	120	125		
His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Phe Ile Gly Gly Ile	130	135	140		
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn	145	150	155	160	
Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met	165	170	175		
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Phe Val	180	185	190		
Val Gly Ser Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala	195	200	205		
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Ser Leu Glu Leu Ser Gly	210	215	220		
Glu Glu Asn Ala Cys Glu Arg Gly Val Ala Gly Glu Lys Ala Lys Thr	225	230	235	240	
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu	245	250	255		
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met	260	265	270		
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Val	275	280	285		
Ile Gly Leu Trp Thr Phe Cys Asn Arg Val	290	295			

<210> 132

<211> 897

<212> DNA

<213> Chlamydia

<400> 132

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gttaaaggctg	ccaagtcctgc	tgccgaattg	accgcaaaata	ttttggaaca	agctggagggc	180
cggggctctct	ccgcacacat	tacagctctcc	caagtgtcca	aaggattagc	ggatgcgaga	240
actgtttctgc	cttttagggaa	tgccctttaac	ggagcggttc	caggaacagt	tcaaatgtcgc	300
caaaagcttct	tcctctacat	gaaagctgct	agtcagaaac	cgcagaaggg	ggataggggg	360
ctcgtagcac	atcttttgtg	gtctcataag	cgcagagcgg	ctgcggctgt	ctgtagcttc	420
atcggaggaa	ttacctacct	cgcgacattc	ggagctatcc	gtccgattct	gtttgtcaac	480
aaaaatgtcg	cgcaaccggt	tcctttcttc	caaaactaaag	caaatatggg	atcttctgtt	540
agctatatatta	tggcgggttaa	ccatgcagcg	tttgtgtgtg	gttctggact	cgctatcagt	600
gcggaaagag	cagattgcga	agcccgctgc	gctcgtattg	cgagagaaga	gtcgtcactc	660
gaattgtcgg	gagaggaaaa	tgcttgtgag	aggagagtcg	ctggagagaa	agccaagacg	720
ttcacgcgca	tcaagtatgc	actcctcact	atgctcgaga	agtttttgga	atgcgtgtcc	780
gacgttttca	aattgtgtgc	gttgctctatt	acaatgggta	ttcgtgcaat	tgtggctgcg	840
ggatgtacgt	tcacttctgc	agttattgga	ttgtggactt	ctctcaacag	agtataaa	897

<210> 133
 <211> 298
 <212> PRT
 <213> Chlamydia

<400> 133
 Met Ala Ala Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
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 Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn
 20 25 30
 Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
 35 40 45
 Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
 50 55 60
 Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
 65 70 75 80
 Thr Val Leu Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
 85 90 95
 Val Gln Ser Ala Gln Ser Phe Phe Ser Tyr Met Lys Ala Ala Ser Gln
 100 105 110
 Lys Pro Gln Glu Gly Asp Glu Gly Leu Val Ala Asp Leu Cys Val Ser
 115 120 125
 His Lys Arg Arg Ala Ala Ala Val Cys Ser Phe Ile Gly Gly Ile
 130 135 140
 Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
 145 150 155 160
 Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
 165 170 175
 Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Phe Val
 180 185 190
 Val Gly Ser Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
 195 200 205
 Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Ser Leu Glu Leu Ser Gly
 210 215 220
 Glu Glu Asn Ala Cys Glu Arg Arg Val Ala Gly Glu Lys Ala Lys Thr
 225 230 235 240
 Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
 245 250 255
 Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
 260 265 270
 Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Val
 275 280 285
 Ile Gly Leu Trp Thr Phe Cys Asn Arg Val
 290 295

<210> 134
 <211> 897
 <212> DNA
 <213> Chlamydia

<400> 134
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 attaaagttg ccaagctctg tgcgaattg accgcaataa ttttgaaca agctggaggc 180
 gcgggtctct ccgcacacat tacagcttcc caagtgtcca aaggattagc ggaatgcgaga 240
 actgttgtcg ctttagggaa tgcctttaac ggagcgttgc caggaacagt tcaaatgctg 300
 caaagcttct tctctacat gaaagctgct agtcagaaaa cgcaagaagg ggaatgaggg 360
 ctcacagcag atctttgtgt gtctcataag cgcagagcgg ctgcggtgtg ctgtagcatc 420

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atcgaggagaa ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac      480
aaaaatgtcgg caaaaacggtt tctttcttcc caaactaaag caaatatggg atcttctgtt      540
agctatatatta tggcggcgttaa ccatgcagcg tctgtggtgg gtgctggact cgctatcagt      600
gcggaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtccgtactc      660
gaaatgccgg gagaggaaaa tgcttgcgag aagaaagtgc ctggagagaa agccaagacg      720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttggg atgcgttgcc      780
gacgttttca aattggtgcc gctgcctatt acaatgggta ttctgtcgat tgtggctgct      840
ggatgtacgt tcacttctgc aattattgga ttgtgcactt tctgcgcag agcataa      897

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<210> 135
 <211> 298
 <212> PRT
 <213> Chlamydia

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<400> 135
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  20          25          30
Lys Thr Lys Gly Met Asp Lys Thr Ile Lys Val Ala Lys Ser Ala Ala
  35          40          45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
  50          55          60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
  65          70          75          80
Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
  85          90          95
Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
  100          105          110
Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
  115          120          125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Ile Ile Gly Gly Ile
  130          135          140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
  145          150          155          160
Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
  165          170          175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
  180          185          190
Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
  195          200          205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Met Pro Gly
  210          215          220
Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr
  225          230          235          240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
  245          250          255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
  260          265          270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
  275          280          285
Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
  290          295

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<210> 136
 <211> 882
 <212> DNA
 <213> Chlamydia

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 ataaaggttg ggaagtctgc tgcgaatta acggcgagta ttttagagca aactgggggg 180
 gcaggagactg atgcacatgt tacggcgccc aagggtgtcta aagcacttgg ggacgcgcga 240
 acagtaatgg ctctagggaa tgtcttcaat gggctctgtc cagcaaccat tcaagtgcg 300
 cgaagtctgc tcgccattt acgagcggcc ggcaaaagag aagaacatg ctccaagggtg 360
 aaagatctct gtgtttctca tagacgaaga gctgcggctg aggtctgtaa tgttattgga 420
 ggagcaactt atattacaac ttctggagcg attctgcga cattactcgt taacaagctt 480
 ctgcgcaaac cattcttttc ctcccaagcc aaagaagggtg tgggagcttc tgttggttat 540
 atcatggcag cgaaccatgc ggcctctgtg cttgggtctg cttaagtat tagcgcagaa 600
 agagcagact gtgaagagcg gtgtgatcgc attcgatgta gtgaggatgg tgaattttgc 660
 gaaggcaata aattaacagc tatttcggaa gagaaggcta gatcatggac tctcattaag 720
 tacagattcc ttactatgat agaaaaacta tttgagatgg tggcggtatg ctccaagtta 780
 attcctttgc caatttcgca tgggaattcgt gctattgttg ctgcgggatg tacgttgact 840
 tctgcagtta ttggcttagg tactttttgg tctagagcat aa 882

<210> 137
 <211> 293
 <212> PRT
 <213> Chlamydia

<400> 137
 Met Ala Ser Val Cys Gly Arg Leu Ser Ala Gly Val Gly Asn Arg Phe
 1 5 10 15
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 Ser Ala Lys Gly Leu Asp Arg Ser Ile Lys Val Gly Lys Ser Ala Ala
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 Glu Leu Thr Ala Ser Ile Leu Glu Gln Thr Gly Gly Ala Gly Thr Asp
 50 55 60
 Ala His Val Thr Ala Ala Lys Val Ser Lys Ala Leu Gly Asp Ala Arg
 65 70 75 80
 Thr Val Met Ala Leu Gly Asn Val Phe Asn Gly Ser Val Pro Ala Thr
 85 90 95
 Ile Gln Ser Ala Arg Ser Cys Leu Ala His Leu Arg Ala Ala Gly Lys
 100 105 110
 Glu Glu Glu Thr Cys Ser Lys Val Lys Asp Leu Cys Val Ser His Arg
 115 120 125
 Arg Arg Ala Ala Ala Glu Ala Cys Asn Val Ile Gly Gly Ala Thr Tyr
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 Ile Thr Thr Phe Gly Ala Ile Arg Pro Thr Leu Leu Val Asn Lys Leu
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 Ser Val Gly Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val Leu Gly
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 Ser Ala Leu Ser Ile Ser Ala Glu Arg Ala Asp Cys Glu Glu Arg Cys
 195 200 205
 Asp Arg Ile Arg Cys Ser Glu Asp Gly Glu Ile Cys Glu Gly Asn Lys
 210 215 220
 Leu Thr Ala Ile Ser Glu Glu Lys Ala Arg Ser Trp Thr Leu Ile Lys
 225 230 235 240
 Tyr Arg Phe Leu Thr Met Ile Glu Lys Leu Phe Glu Met Val Ala Asp
 245 250 255
 Ile Phe Lys Leu Ile Pro Leu Pro Ile Ser His Gly Ile Arg Ala Ile
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<210> 139
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<400> 148
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<400> 157
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Leu Lys Gln Ile Trp
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<210> 158
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<400> 163
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<210> 166
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<210> 167
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<210> 169
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<213> Chlamydia

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<211> 4593

<212> DNA

<213> Chlamydia

<400> 172

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<211> 5331

<212> DNA

<213> Chlamydia

<400> 173

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<212> DNA

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<400> 174

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tctgtctatg	gaggtaaat	cctgtatttc	ttgtccaata	agcaacatgg	ttgggcactt	4680
ccctttccata	tacaaggagt	cggtctctat	ggacataatta	aaactgtatc	aaacaaactt	4740
taccccttcta	tccatgaaga	aaataaaggga	gattgggaag	atttaggtat	tgtacgggat	4800
ctctgtattct	ctatggatct	taagaacact	tctaaagatt	cttctaaacg	gatcactgtc	4860
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ccaagacact	tcgatgattg	tgcttacaga	aatctgtcgc	ttcctgtggg	atgcgctgtc	4980
gaaggagcta	tactgaactg	taataattct	atgtataata	agcttgcatt	agcctacatg	5040

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cctctctatct acagaaataa tctgtctgtt aaatatcggt tattgtcttc gaatgaagct 5100
ggtaaggtta tctgaggagt gccaaactaga acctctgcta gagcagaata cagtactcaa 5160
ctatatcttg gtccctctct gactctctac ggaaactata ctatcgatgt aggcgatgat 5220
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<210> 175

<211> 880

<212> PRT

<213> Chlamydia

<220>

<221> VARIANT

<222> (1)...(880)

<223> Xaa = Any Amino Acid

<400> 175

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Ile Leu Ser Ser Thr Ala Val Leu Phe Gly Gln Asp Pro Leu Gly Glu
20 25 30
Thr Ala Leu Leu Thr Lys Asn Pro Asn His Val Val Cys Thr Phe Phe
35 40 45
Glu Asp Cys Thr Met Glu Ser Leu Phe Pro Ala Leu Cys Ala His Ala
50 55 60
Ser Gln Asp Asp Pro Leu Tyr Val Leu Gly Asn Ser Tyr Cys Trp Phe
65 70 75 80
Val Ser Lys Leu His Ile Thr Asp Pro Lys Glu Ala Leu Phe Lys Glu
85 90 95
Lys Gly Asp Leu Ser Ile Gln Asn Phe Arg Phe Leu Ser Phe Thr Asp
100 105 110
Cys Ser Ser Lys Glu Ser Ser Pro Ser Ile Ile His Gln Lys Asn Gly
115 120 125
Gln Leu Ser Leu Arg Asn Asn Gly Ser Met Ser Phe Cys Arg Asn His
130 135 140
Ala Glu Gly Ser Gly Gly Ala Ile Ser Ala Asp Ala Phe Ser Leu Gln
145 150 155 160
His Asn Tyr Leu Phe Thr Ala Phe Glu Glu Asn Ser Ser Lys Gly Asn
165 170 175
Gly Gly Ala Ile Gln Ala Gln Thr Phe Ser Leu Ser Arg Asn Val Ser
180 185 190
Pro Ile Ser Phe Ala Arg Asn Arg Ala Asp Leu Asn Gly Gly Ala Ile
195 200 205
Cys Cys Ser Asn Leu Ile Cys Ser Gly Asn Val Asn Pro Leu Phe Phe
210 215 220
Thr Gly Asn Ser Ala Thr Asn Gly Gly Ala Ile Cys Cys Ile Ser Asp
225 230 235 240
Leu Asn Thr Ser Glu Lys Gly Ser Leu Ser Leu Ala Cys Asn Gln Glu
245 250 255
Thr Leu Phe Ala Ser Asn Ser Ala Lys Glu Lys Gly Gly Ala Ile Tyr
260 265 270
Ala Lys His Met Val Leu Arg Tyr Asn Gly Pro Val Ser Phe Ile Asn
275 280 285
Asn Ser Ala Lys Ile Gly Gly Ala Ile Ala Ile Gln Ser Gly Gly Ser
290 295 300
Leu Ser Ile Leu Ala Gly Glu Gly Ser Val Leu Phe Gln Asn Asn Ser
305 310 315 320

```

Gln	Arg	Thr	Ser	Asp	Gln	Gly	Leu	Val	Arg	Asn	Ala	Ile	Tyr	Leu	Xaa
Lys	Asp	Ala	Ile	325	Leu	Ser	Ser	Leu	330	Ala	Arg	Asn	Gly	335	Ile
Phe	Phe	Asp	Pro	340	Ile	Val	Gln	Glu	345	Ser	Ser	Ser	Lys	Glu	Ser
Pro	Ser	Ser	Leu	355	Gln	Ala	Ser	Val	360	Thr	Ser	Pro	Thr	Pro	Ala
Ser	Pro	Leu	Val	370	Ile	Gln	Thr	Ser	375	Ala	Asn	Arg	Ser	Val	Ile
Ser	Glu	Arg	Leu	385	Ser	Glu	Glu	Glu	390	Lys	Thr	Pro	Asp	Asn	Leu
Gln	Leu	Gln	Gln	400	Pro	Ile	Glu	Leu	405	Lys	Ser	Gly	Arg	Leu	Val
Asp	Arg	Ala	Val	415	Leu	Ser	Ala	Pro	420	Ser	Ser	Leu	Ser	Gln	Ala
Leu	Leu	Ile	Met	425	Glu	Ala	Gly	Thr	430	Ser	Leu	Lys	Thr	Ser	Ser
Lys	Leu	Ala	Thr	440	Leu	Ser	Ile	Pro	445	Leu	His	Ser	Leu	Asp	Thr
Ser	Val	Thr	Ile	450	His	Ala	Pro	Asn	455	Leu	Ser	Ile	Gln	Lys	Ile
Ser	Asn	Ser	Gly	460	Asp	Glu	Asn	Phe	465	Tyr	Glu	Asn	Val	Glu	Leu
Lys	Glu	Gln	Asn	470	Asn	Ile	Pro	Leu	475	Leu	Thr	Leu	Pro	Lys	Glu
His	Leu	His	Leu	480	Pro	Asp	Gly	Asn	485	Leu	Ser	Ser	His	Phe	Gly
Gly	Asp	Trp	Thr	490	Ser	Trp	Lys	Asp	495	Ser	Asp	Glu	Gly	His	Ser
Ile	Ala	Asn	Trp	500	Pro	Lys	Asn	Tyr	505	Val	Pro	His	Pro	Glu	Arg
Ser	Thr	Leu	Val	510	Ala	Asn	Thr	Leu	515	Trp	Asn	Thr	Tyr	Ser	Asp
Ala	Val	Gln	Ser	520	Met	Ile	Asn	Thr	525	Ala	His	Gly	Gly	Ala	Tyr
Phe	Gly	Thr	Trp	530	Gly	Ser	Ala	Val	535	Ser	Asn	Leu	Phe	Tyr	Val
Ser	Ser	Gly	Lys	540	Pro	Ile	Asp	Asn	545	Trp	His	Arg	Ser	Leu	Gly
Leu	Phe	Gly	Ile	550	Ser	Thr	His	Ser	555	Leu	Asp	Asp	His	Ser	Phe
Ala	Ala	Gly	Gln	560	Leu	Leu	Gly	Lys	565	Ser	Ser	Asp	Ser	Phe	Ile
Thr	Glu	Thr	Thr	570	Ser	Tyr	Ile	Ala	575	Val	Gln	Ala	Gln	Leu	Ala
Ser	Leu	Met	Lys	580	Ile	Ser	Ala	Gln	585	Ala	Cys	Tyr	Asn	Glu	Ser
Glu	Leu	Lys	Thr	590	Tyr	Arg	Ser	Phe	595	Ser	Lys	Glu	Gly	Phe	Gly
Trp	His	Ser	Val	600	Ala	Val	Ser	Gly	605	Glu	Val	Cys	Ala	Ser	Ile
Val	Ser	Asn	Gly	610	Ser	Gly	Leu	Phe	615	Ser	Ser	Phe	Ser	Ile	Phe
Leu	Gln	Gly	Phe	620	Ser	Gly	Thr	Gln	625	Asp	Gly	Phe	Glu	Ser	Ser
Glu	Ile	Arg	Ser	630	Phe	Ser	Ala	Ser	635	Ser	Phe	Arg	Asn	Ile	Ser
				640					645						
				650					655						
				660					665						
				670					675						
				680					685						
				690					695						
				700					705						
				710					715						
				720					725						
				730					735						
				740					745						
				750					755						
				760					765						

```

Ile Gly Ile Thr Phe Glu Lys Lys Ser Gln Lys Thr Arg Thr Tyr Tyr
785             790             795             800
Tyr Phe Leu Gly Ala Tyr Ile Gln Asp Leu Lys Arg Asp Val Glu Ser
            805             810             815
Gly Pro Val Val Leu Leu Lys Asn Ala Val Ser Trp Asp Ala Pro Met
            820             825             830
Ala Asn Leu Asp Ser Arg Ala Tyr Met Phe Arg Leu Thr Asn Gln Arg
            835             840             845
Ala Leu His Arg Leu Gln Thr Leu Leu Asn Val Ser Cys Val Leu Arg
            850             855             860
Gly Gln Ser His Ser Tyr Ser Leu Asp Leu Gly Thr Thr Tyr Arg Phe
865             870             875             880

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<210> 176

<211> 982

<212> PRT

<213> Chlamydia

<220>

<221> VARIANT

<222> (1)...(982)

<223> Xaa = Any Amino Acid

<400> 176

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Met Ile Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val Ser Phe
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Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala
            20             25             30
Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Leu Pro
35             40             45
Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg
50             55             60
Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala
65             70             75             80
Ala Leu Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr Ile Glu Gly Phe
            85             90             95
Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val Leu Pro
100            105            110
Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr Thr Ser Thr
115            120            125
Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu Asn
130            135            140
Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp Gly Gly
145            150            155            160
Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys Leu Cys
165            170            175
Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys Gln Val
180            185            190
Val Thr Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala Phe Val
195            200            205
Ala Asn Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val Gln Asp
210            215            220
Gly Gln Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro Val Val
225            230            235            240
Ser Phe Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val Ala Arg
245            250            255
Val Gly Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu Asn Asn
260            265            270

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Gly Lys Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr Ile Ala
 275 280 285
 Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr Ser Asn Asn Tyr
 290 295 300
 Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala Gly Ser
 305 310 315 320
 Asn Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val Phe Phe
 325 330 335
 Ser Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile Tyr Ala Lys Lys
 340 345 350
 Leu Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu Arg Asn Ile Ala
 355 360 365
 Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly Glu Leu Ser Leu
 370 375 380
 Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn Leu Lys Arg Thr
 385 390 395 400
 Ala Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser Ser Gln
 405 410 415
 Ala Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr Leu Arg Ala Lys
 420 425 430
 Ala Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu Met Ala Asn Gly
 435 440 445
 Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys Ile Asn Asp Gly
 450 455 460
 Glu Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly Ser Ser Thr Leu
 465 470 475 480
 Tyr Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg Glu Lys
 485 490 495
 Ala Lys Leu Ser Val Asn Ser Leu Ser Gln Thr Gly Gly Ser Leu Tyr
 500 505 510
 Met Glu Ala Gly Ser Thr Leu Asp Phe Val Thr Pro Gln Pro Pro Gln
 515 520 525
 Gln Pro Pro Ala Ala Asn Gln Leu Ile Thr Leu Ser Asn Leu His Leu
 530 535 540
 Ser Leu Ser Ser Leu Leu Ala Asn Asn Ala Val Thr Asn Pro Pro Thr
 545 550 555 560
 Asn Pro Pro Ala Gln Asp Ser His Pro Ala Val Ile Gly Ser Thr Thr
 565 570 575
 Ala Gly Ser Val Thr Ile Ser Gly Pro Ile Phe Phe Glu Asp Leu Asp
 580 585 590
 Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu Gly Ser Asn Gln Lys Ile
 595 600 605
 Asn Val Leu Lys Leu Gln Leu Gly Thr Lys Pro Pro Ala Asn Ala Pro
 610 615 620
 Ser Asp Leu Thr Leu Gly Asn Glu Met Pro Lys Tyr Gly Tyr Gln Gly
 625 630 635 640
 Ser Trp Lys Leu Ala Trp Asp Pro Asn Thr Ala Asn Asn Gly Pro Tyr
 645 650 655
 Thr Leu Lys Ala Thr Trp Thr Lys Thr Gly Tyr Asn Pro Gly Pro Glu
 660 665 670
 Arg Val Ala Ser Leu Val Pro Asn Ser Leu Trp Gly Ser Ile Leu Asp
 675 680 685
 Ile Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val Asp Gly Arg Ser
 690 695 700
 Tyr Cys Arg Gly Leu Trp Val Ser Gly Val Ser Asn Phe Phe Tyr His
 705 710 715 720
 Asp Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile Ser Gly Gly Tyr
 725 730 735

[illegible]

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<210> 177
<211> 964
<212> PRT
<213> Chlamydia
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Met	Lys	Lys	Ala	Phe	Phe	Phe	Phe	Leu	Ile	Gly	Asn	Ser	Leu	Ser	Gly
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Leu	Ala	Arg	Glu	Val	Pro	Ser	Arg	Ile	Phe	Leu	Met	Pro	Asn	Ser	Val
			20					25					30		
Pro	Asp	Pro	Thr	Lys	Glu	Ser	Leu	Ser	Asn	Lys	Ile	Ser	Leu	Thr	Gly
			35				40					45			
Asp	Thr	His	Asn	Leu	Thr	Asn	Cys	Tyr	Leu	Asp	Asn	Leu	Arg	Tyr	Ile
	50					55					60				
Leu	Ala	Ile	Leu	Gln	Lys	Thr	Pro	Asn	Glu	Gly	Ala	Ala	Val	Thr	Ile
65				70					75					80	
Thr	Asp	Tyr	Leu	Ser	Phe	Phe	Asp	Thr	Gln	Lys	Glu	Gly	Ile	Tyr	Phe
			85					90					95		
Ala	Lys	Asn	Leu	Thr	Pro	Glu	Ser	Gly	Gly	Ala	Ile	Gly	Tyr	Ala	Ser
			100					105					110		
Pro	Asn	Ser	Pro	Thr	Val	Glu	Ile	Arg	Asp	Thr	Ile	Gly	Pro	Val	Ile
			115				120					125			
Phe	Glu	Asn	Asn	Thr	Cys	Cys	Arg	Leu	Phe	Thr	Trp	Arg	Asn	Pro	Tyr
	130					135					140				
Ala	Ala	Asp	Lys	Ile	Arg	Glu	Gly	Gly	Ala	Ile	His	Ala	Gln	Asn	Leu

145 150 155 160
 Tyr Ile Asn His Asn His Asp Val Val Gly Phe Met Lys Asn Phe Ser
 165 170 175
 Tyr Val Gln Gly Gly Ala Ile Ser Thr Ala Asn Thr Phe Val Val Ser
 180 185 190
 Glu Asn Gln Ser Cys Phe Leu Phe Met Asp Asn Ile Cys Ile Gln Thr
 195 200 205
 Asn Thr Ala Gly Lys Gly Gly Ala Ile Tyr Ala Gly Thr Ser Asn Ser
 210 215 220
 Phe Glu Ser Asn Asn Cys Asp Leu Phe Phe Ile Asn Asn Ala Cys Cys
 225 230 235 240
 Ala Gly Gly Ala Ile Phe Ser Pro Ile Cys Ser Leu Thr Gly Asn Arg
 245 250 255
 Gly Asn Ile Val Phe Tyr Asn Asn Arg Cys Phe Lys Asn Val Glu Thr
 260 265 270
 Ala Ser Ser Glu Ala Ser Asp Gly Gly Ala Ile Lys Val Thr Thr Arg
 275 280 285
 Leu Asp Val Thr Gly Asn Arg Gly Arg Ile Phe Phe Ser Asp Asn Ile
 290 295 300
 Thr Lys Asn Tyr Gly Gly Ala Ile Tyr Ala Pro Val Val Thr Leu Val
 305 310 315 320
 Asp Asn Gly Pro Thr Tyr Phe Ile Asn Asn Ile Ala Asn Asn Lys Gly
 325 330 335
 Gly Ala Ile Tyr Ile Asp Gly Thr Ser Asn Ser Lys Ile Ser Ala Asp
 340 345 350
 Arg His Ala Ile Ile Phe Asn Glu Asn Ile Val Thr Asn Val Thr Asn
 355 360 365
 Ala Asn Gly Thr Ser Thr Ser Ala Asn Pro Pro Arg Arg Asn Ala Ile
 370 375 380
 Thr Val Ala Ser Ser Ser Gly Glu Ile Leu Leu Gly Ala Gly Ser Ser
 385 390 395 400
 Gln Asn Leu Ile Phe Tyr Asp Pro Ile Glu Val Ser Asn Ala Gly Val
 405 410 415
 Ser Val Ser Phe Asn Lys Glu Ala Asp Gln Thr Gly Ser Val Val Phe
 420 425 430
 Ser Gly Ala Thr Val Asn Ser Ala Asp Phe His Gln Arg Asn Leu Gln
 435 440 445
 Thr Lys Thr Pro Ala Pro Leu Thr Leu Ser Asn Gly Phe Leu Cys Ile
 450 455 460
 Glu Asp His Ala Gln Leu Thr Val Asn Arg Phe Thr Gln Thr Gly Gly
 465 470 475 480
 Val Val Ser Leu Gly Asn Gly Ala Val Leu Ser Cys Tyr Lys Asn Gly
 485 490 495
 Thr Gly Asp Ser Ala Ser Asn Ala Ser Ile Thr Leu Lys His Ile Gly
 500 505 510
 Leu Asn Leu Ser Ser Ile Leu Lys Ser Gly Ala Glu Ile Pro Leu Leu
 515 520 525
 Trp Val Glu Pro Thr Asn Asn Ser Asn Asn Tyr Thr Ala Asp Thr Ala
 530 535 540
 Ala Thr Phe Ser Leu Ser Asp Val Lys Leu Ser Leu Ile Asp Asp Tyr
 545 550 555 560
 Gly Asn Ser Pro Tyr Glu Ser Thr Asp Leu Thr His Ala Leu Ser Ser
 565 570 575
 Gln Pro Met Leu Ser Ile Ser Glu Ala Ser Asp Asn Gln Leu Gln Ser
 580 585 590
 Glu Asn Ile Asp Phe Ser Gly Leu Asn Val Pro His Tyr Gly Trp Gln
 595 600 605
 Gly Leu Trp Thr Trp Gly Trp Ala Lys Thr Gln Asp Pro Glu Pro Ala


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        610                615                620
Ser Ser Ala Thr Ile Thr Asp Pro Gln Lys Ala Asn Arg Phe His Arg
625                630                635                640
Thr Leu Leu Leu Thr Trp Leu Pro Ala Gly Tyr Val Pro Ser Pro Lys
        645                650                655
His Arg Ser Pro Leu Ile Ala Asn Thr Leu Trp Gly Asn Met Leu Leu
        660                665                670
Ala Thr Glu Ser Leu Lys Asn Ser Ala Glu Leu Thr Pro Ser Gly His
        675                680                685
Pro Phe Trp Gly Ile Thr Gly Gly Gly Leu Gly Met Met Val Tyr Gln
        690                695                700
Asp Pro Arg Glu Asn His Pro Gly Phe His Met Arg Ser Ser Gly Tyr
705                710                715                720
Ser Ala Gly Met Ile Ala Gly Gln Thr His Thr Phe Ser Leu Lys Phe
        725                730                735
Ser Gln Thr Tyr Thr Lys Leu Asn Glu Arg Tyr Ala Lys Asn Asn Val
        740                745                750
Ser Ser Lys Asn Tyr Ser Cys Gln Gly Glu Met Leu Phe Ser Leu Gln
        755                760                765
Glu Gly Phe Leu Leu Thr Lys Leu Val Gly Leu Tyr Ser Tyr Gly Asp
        770                775                780
His Asn Cys His His Phe Tyr Thr Gln Gly Glu Asn Leu Thr Ser Gln
785                790                795                800
Gly Thr Phe Arg Ser Gln Thr Met Gly Gly Ala Val Phe Phe Asp Leu
        805                810                815
Pro Met Lys Pro Phe Gly Ser Thr His Ile Leu Thr Ala Pro Phe Leu
        820                825                830
Gly Ala Leu Gly Ile Tyr Ser Ser Leu Ser His Phe Thr Glu Val Gly
        835                840                845
Ala Tyr Pro Arg Ser Phe Ser Thr Lys Thr Pro Leu Ile Asn Val Leu
        850                855                860
Val Pro Ile Gly Val Lys Gly Ser Phe Met Asn Ala Thr His Arg Pro
865                870                875                880
Gln Ala Trp Thr Val Glu Leu Ala Tyr Gln Pro Val Leu Tyr Arg Gln
        885                890                895
Glu Pro Gly Ile Ala Thr Gln Leu Leu Ala Ser Lys Gly Ile Trp Phe
        900                905                910
Gly Ser Gly Ser Pro Ser Ser Arg His Ala Met Ser Tyr Lys Ile Ser
        915                920                925
Gln Gln Thr Gln Pro Leu Ser Trp Leu Thr Leu His Phe Gln Tyr His
        930                935                940
Gly Phe Tyr Ser Ser Ser Thr Phe Cys Asn Tyr Leu Asn Gly Glu Ile
945                950                955                960
Ala Leu Arg Phe

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<210> 178

<211> 1530

<212> PRT

<213> Chlamydia

<400> 178

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Met Ser Ser Glu Lys Asp Ile Lys Ser Thr Cys Ser Lys Phe Ser Leu
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Ser Val Val Ala Ala Ile Leu Ala Ser Val Ser Gly Leu Ala Ser Cys
        20                25                30
Val Asp Leu His Ala Gly Gly Gln Ser Val Asn Glu Leu Val Tyr Val
        35                40                45

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Gly Pro Gln Ala Val Leu Leu Leu Asp Gln Ile Arg Asp Leu Phe Val
 50 55 60
 Gly Ser Lys Asp Ser Gln Ala Glu Gly Gln Tyr Arg Leu Ile Val Gly
 65 70 75 80
 Asp Pro Ser Ser Phe Gln Glu Lys Asp Ala Asp Thr Leu Pro Gly Lys
 85 90 95
 Val Glu Gln Ser Thr Leu Phe Ser Val Thr Asn Pro Val Val Phe Gln
 100 105 110
 Gly Val Asp Gln Gln Asp Gln Val Ser Ser Gln Gly Leu Ile Cys Ser
 115 120 125
 Phe Thr Ser Ser Asn Leu Asp Ser Pro Arg Asp Gly Glu Ser Phe Leu
 130 135 140
 Gly Ile Ala Phe Val Gly Asp Ser Ser Lys Ala Gly Ile Thr Leu Thr
 145 150 155 160
 Asp Val Lys Ala Ser Leu Ser Gly Ala Ala Leu Tyr Ser Thr Glu Asp
 165 170 175
 Leu Ile Phe Glu Lys Ile Lys Gly Gly Leu Glu Phe Ala Ser Cys Ser
 180 185 190
 Ser Leu Glu Gln Gly Gly Ala Cys Ala Ala Gln Ser Ile Leu Ile His
 195 200 205
 Asp Cys Gln Gly Leu Gln Val Lys His Cys Thr Thr Ala Val Asn Ala
 210 215 220
 Glu Gly Ser Ser Ala Asn Asp His Leu Gly Phe Gly Gly Ala Phe
 225 230 235 240
 Phe Val Thr Gly Ser Leu Ser Gly Glu Lys Ser Leu Tyr Met Pro Ala
 245 250 255
 Gly Asp Met Val Val Ala Asn Cys Asp Gly Ala Ile Ser Phe Glu Gly
 260 265 270
 Asn Ser Ala Asn Phe Ala Asn Gly Gly Ala Ile Ala Ala Ser Gly Lys
 275 280 285
 Val Leu Phe Val Ala Asn Asp Lys Lys Thr Ser Phe Ile Glu Asn Arg
 290 295 300
 Ala Leu Ser Gly Gly Ala Ile Ala Ala Ser Ser Asp Ile Ala Phe Gln
 305 310 315 320
 Asn Cys Ala Glu Leu Val Phe Lys Gly Asn Cys Ala Ile Gly Thr Glu
 325 330 335
 Asp Lys Gly Ser Leu Gly Gly Gly Ala Ile Ser Ser Leu Gly Thr Val
 340 345 350
 Leu Leu Gln Gly Asn His Gly Ile Thr Cys Asp Lys Asn Glu Ser Ala
 355 360 365
 Ser Gln Gly Gly Ala Ile Phe Gly Lys Asn Cys Gln Ile Ser Asp Asn
 370 375 380
 Glu Gly Pro Val Val Phe Arg Asp Ser Thr Ala Cys Leu Gly Gly Gly
 385 390 395 400
 Ala Ile Ala Ala Gln Glu Ile Val Ser Ile Gln Asn Asn Gln Ala Gly
 405 410 415
 Ile Ser Phe Glu Gly Gly Lys Ala Ser Phe Gly Gly Gly Ile Ala Cys
 420 425 430
 Gly Ser Phe Ser Ser Ala Gly Gly Ala Ser Val Leu Gly Thr Ile Asp
 435 440 445
 Ile Ser Lys Asn Leu Gly Ala Ile Ser Phe Ser Arg Thr Leu Cys Thr
 450 455 460
 Thr Ser Asp Leu Gly Gln Met Glu Tyr Gln Gly Gly Ala Leu Phe
 465 470 475 480
 Gly Glu Asn Ile Ser Leu Ser Glu Asn Ala Gly Val Leu Thr Phe Lys
 485 490 495
 Asp Asn Ile Val Lys Thr Phe Ala Ser Asn Gly Lys Ile Leu Gly Gly
 500 505 510

Gly Ala Ile Leu Ala Thr Gly Lys Val Glu Ile Thr Asn Asn Ser Gly
 515 520 525
 Gly Ile Ser Phe Thr Gly Asn Ala Arg Ala Pro Gln Ala Leu Pro Thr
 530 535 540
 Gln Glu Glu Phe Pro Leu Phe Ser Lys Lys Glu Gly Arg Pro Leu Ser
 545 550 555 560
 Ser Gly Tyr Ser Gly Gly Ala Ile Leu Gly Arg Glu Val Ala Ile
 565 570 575
 Leu His Asn Ala Ala Val Val Phe Glu Gln Asn Arg Leu Gln Cys Ser
 580 585 590
 Glu Glu Glu Ala Thr Leu Leu Gly Cys Cys Gly Gly Gly Ala Val His
 595 600 605
 Gly Met Asp Ser Thr Ser Ile Val Gly Asn Ser Ser Val Arg Phe Gly
 610 615 620
 Asn Asn Tyr Ala Met Gly Gln Gly Val Ser Gly Gly Ala Leu Leu Ser
 625 630 635 640
 Lys Thr Val Gln Leu Ala Gly Asn Gly Ser Val Asp Phe Ser Arg Asn
 645 650 655
 Ile Ala Ser Leu Gly Gly Ala Leu Gln Ala Ser Glu Gly Asn Cys
 660 665 670
 Glu Leu Val Asp Asn Gly Tyr Val Leu Phe Arg Asp Asn Arg Gly Arg
 675 680 685
 Val Tyr Gly Gly Ala Ile Ser Cys Leu Arg Gly Asp Val Val Ile Ser
 690 695 700
 Gly Asn Lys Gly Arg Val Glu Phe Lys Asp Asn Ile Ala Thr Arg Leu
 705 710 715 720
 Tyr Val Glu Glu Thr Val Glu Lys Val Glu Glu Val Glu Pro Ala Pro
 725 730 735
 Glu Gln Lys Asp Asn Asn Glu Leu Ser Phe Leu Gly Ser Val Glu Gln
 740 745 750
 Ser Phe Ile Thr Ala Ala Asn Gln Ala Leu Phe Ala Ser Glu Asp Gly
 755 760 765
 Asp Leu Ser Pro Glu Ser Ser Ile Ser Ser Glu Glu Leu Ala Lys Arg
 770 775 780
 Arg Glu Cys Ala Gly Gly Ala Ile Phe Ala Lys Arg Val Arg Ile Val
 785 790 795 800
 Asp Asn Gln Glu Ala Val Val Phe Ser Asn Asn Phe Ser Asp Ile Tyr
 805 810 815
 Gly Gly Ala Ile Phe Thr Gly Ser Leu Arg Glu Glu Asp Lys Leu Asp
 820 825 830
 Gly Gln Ile Pro Glu Val Leu Ile Ser Gly Asn Ala Gly Asp Val Val
 835 840 845
 Phe Ser Gly Asn Ser Ser Lys Arg Asp Glu His Leu Pro His Thr Gly
 850 855 860
 Gly Gly Ala Ile Cys Thr Gln Asn Leu Thr Ile Ser Gln Asn Thr Gly
 865 870 875 880
 Asn Val Leu Phe Tyr Asn Asn Val Ala Cys Ser Gly Gly Ala Val Arg
 885 890 895
 Ile Glu Asp His Gly Asn Val Leu Leu Glu Ala Phe Gly Gly Asp Ile
 900 905 910
 Val Phe Lys Gly Asn Ser Ser Phe Arg Ala Gln Gly Ser Asp Ala Ile
 915 920 925
 Tyr Phe Ala Gly Lys Glu Ser His Ile Thr Ala Leu Asn Ala Thr Glu
 930 935 940
 Gly His Ala Ile Val Phe His Asp Ala Leu Val Phe Glu Asn Leu Lys
 945 950 955 960
 Glu Arg Lys Ser Ala Glu Val Leu Leu Ile Asn Ser Arg Glu Asn Pro
 965 970 975

Gly Tyr Thr Gly Ser Ile Arg Phe Leu Glu Ala Glu Ser Lys Val Pro
 980 985 990
 Gln Cys Ile His Val Gln Gln Gly Ser Leu Glu Leu Leu Asn Gly Ala
 995 1000 1005
 Thr Leu Cys Ser Tyr Gly Phe Lys Gln Asp Ala Gly Ala Lys Leu Val
 1010 1015 1020
 Leu Ala Ala Gly Ser Lys Leu Lys Ile Leu Asp Ser Gly Thr Pro Val
 1025 1030 1035 1040
 Gln Gly His Ala Ile Ser Lys Pro Glu Ala Glu Ile Glu Ser Ser Ser
 1045 1050 1055
 Glu Pro Glu Gly Ala His Ser Leu Trp Ile Ala Lys Asn Ala Gln Thr
 1060 1065 1070
 Thr Val Pro Met Val Asp Ile His Thr Ile Ser Val Asp Leu Ala Ser
 1075 1080 1085
 Phe Ser Ser Ser Gln Gln Glu Gly Thr Val Glu Ala Pro Gln Val Ile
 1090 1095 1100
 Val Pro Gly Gly Ser Tyr Val Arg Ser Gly Glu Leu Asn Leu Glu Leu
 1105 1110 1115 1120
 Val Asn Thr Thr Gly Thr Gly Tyr Glu Asn His Ala Leu Leu Lys Asn
 1125 1130 1135
 Glu Ala Lys Val Pro Leu Met Ser Phe Val Ala Ser Ser Asp Glu Ala
 1140 1145 1150
 Ser Ala Glu Ile Ser Asn Leu Ser Val Ser Asp Leu Gln Ile His Val
 1155 1160 1165
 Ala Thr Pro Glu Ile Glu Glu Asp Thr Tyr Gly His Met Gly Asp Trp
 1170 1175 1180
 Ser Glu Ala Lys Ile Gln Asp Gly Thr Leu Val Ile Asn Trp Asn Pro
 1185 1190 1195 1200
 Thr Gly Tyr Arg Leu Asp Pro Gln Lys Ala Gly Ala Leu Val Phe Asn
 1205 1210 1215
 Ala Leu Trp Glu Glu Gly Ala Val Leu Ser Ala Leu Lys Asn Ala Arg
 1220 1225 1230
 Phe Ala His Asn Leu Thr Ala Gln Arg Met Glu Phe Asp Tyr Ser Thr
 1235 1240 1245
 Asn Val Trp Gly Phe Ala Phe Gly Gly Phe Arg Thr Leu Ser Ala Glu
 1250 1255 1260
 Asn Leu Val Ala Ile Asp Gly Tyr Lys Gly Ala Tyr Gly Gly Ala Ser
 1265 1270 1275 1280
 Ala Gly Val Asp Ile Gln Leu Met Glu Asp Phe Val Leu Gly Val Ser
 1285 1290 1295
 Gly Ala Ala Phe Leu Gly Lys Met Asp Ser Gln Lys Phe Asp Ala Glu
 1300 1305 1310
 Val Ser Arg Lys Gly Val Val Gly Ser Val Tyr Thr Gly Phe Leu Ala
 1315 1320 1325
 Gly Ser Trp Phe Phe Lys Gly Gln Tyr Ser Leu Gly Glu Thr Gln Asn
 1330 1335 1340
 Asp Met Lys Thr Arg Tyr Gly Val Leu Gly Glu Ser Ser Ala Ser Trp
 1345 1350 1355 1360
 Thr Ser Arg Gly Val Leu Ala Asp Ala Leu Val Glu Tyr Arg Ser Leu
 1365 1370 1375
 Val Gly Pro Val Arg Pro Thr Phe Tyr Ala Leu His Phe Asn Pro Tyr
 1380 1385 1390
 Val Glu Val Ser Tyr Ala Ser Met Lys Phe Pro Gly Phe Thr Glu Gln
 1395 1400 1405
 Gly Arg Glu Ala Arg Ser Phe Glu Asp Ala Ser Leu Thr Asn Ile Thr
 1410 1415 1420
 Ile Pro Leu Gly Met Lys Phe Glu Leu Ala Phe Ile Lys Gly Gln Phe
 1425 1430 1435 1440

Ser Glu Val Asn Ser Leu Gly Ile Ser Tyr Ala Trp Glu Ala Tyr Arg
 1445 1450 1455
 Lys Val Glu Gly Gly Ala Val Gln Leu Leu Glu Ala Gly Phe Asp Trp
 1460 1465 1470
 Glu Gly Ala Pro Met Asp Leu Pro Arg Gln Glu Leu Arg Val Ala Leu
 1475 1480 1485
 Glu Asn Asn Thr Glu Trp Ser Ser Tyr Phe Ser Thr Val Leu Gly Leu
 1490 1495 1500
 Thr Ala Phe Cys Gly Gly Phe Thr Ser Thr Asp Ser Lys Leu Gly Tyr
 1505 1510 1515 1520
 Glu Ala Asn Thr Gly Leu Arg Leu Ile Phe
 1525 1530

<210> 179

<211> 1776

<212> PRT

<213> Chlamydia

<400> 179

Ala Ile Met Lys Phe Met Ser Ala Thr Ala Val Phe Ala Ala Val Leu
 1 5 10 15
 Ser Ser Val Thr Glu Ala Ser Ser Ile Gln Asp Gln Ile Lys Asn Thr
 20 25 30
 Asp Cys Asn Val Ser Lys Val Gly Tyr Ser Thr Ser Gln Ala Phe Thr
 35 40 45
 Asp Met Met Leu Ala Asp Asn Thr Glu Tyr Arg Ala Ala Asp Ser Val
 50 55 60
 Ser Phe Tyr Asp Phe Ser Thr Ser Ser Gly Leu Pro Arg Lys His Leu
 65 70 75 80
 Ser Ser Ser Ser Glu Ala Ser Pro Thr Thr Glu Gly Val Ser Ser Ser
 85 90 95
 Ser Ser Gly Glu Asn Thr Glu Asn Ser Gln Asp Ser Ala Pro Ser Ser
 100 105 110
 Gly Glu Thr Asp Lys Lys Thr Glu Glu Glu Leu Asp Asn Gly Gly Ile
 115 120 125
 Ile Tyr Ala Arg Glu Lys Leu Thr Ile Ser Glu Ser Gln Asp Ser Leu
 130 135 140
 Ser Asn Pro Ser Ile Glu Leu His Asp Asn Ser Phe Phe Phe Gly Glu
 145 150 155 160
 Gly Glu Val Ile Phe Asp His Arg Val Ala Leu Lys Asn Gly Gly Ala
 165 170 175
 Ile Tyr Gly Glu Lys Glu Val Val Phe Glu Asn Ile Lys Ser Leu Leu
 180 185 190
 Val Glu Val Asn Ile Ser Val Glu Lys Gly Gly Ser Val Tyr Ala Lys
 195 200 205
 Glu Arg Val Ser Leu Glu Asn Val Thr Glu Ala Thr Phe Ser Ser Asn
 210 215 220
 Gly Gly Glu Gln Gly Gly Gly Ile Tyr Ser Glu Gln Asp Met Leu
 225 230 235 240
 Ile Ser Asp Cys Asn Asn Val His Phe Gln Gly Asn Ala Ala Gly Ala
 245 250 255
 Thr Ala Val Lys Gln Cys Leu Asp Glu Glu Met Ile Val Leu Leu Thr
 260 265 270
 Glu Cys Val Asp Ser Leu Ser Glu Asp Thr Leu Asp Ser Thr Pro Glu
 275 280 285
 Thr Glu Gln Thr Lys Ser Asn Gly Asn Gln Asp Gly Ser Ser Glu Thr
 290 295 300
 Lys Asp Thr Gln Val Ser Glu Ser Pro Glu Ser Thr Pro Ser Pro Asp

305 310 315 320
 Asp Val Leu Gly Lys Gly Gly Ile Tyr Thr Glu Lys Ser Leu Thr
 325 330 335
 Ile Thr Gly Ile Thr Gly Thr Ile Asp Phe Val Ser Asn Ile Ala Thr
 340 345 350
 Asp Ser Gly Ala Gly Val Phe Thr Lys Glu Asn Leu Ser Cys Thr Asn
 355 360 365
 Thr Asn Ser Leu Gln Phe Leu Lys Asn Ser Ala Gly Gln His Gly Gly
 370 375 380
 Gly Ala Tyr Val Thr Gln Thr Met Ser Val Thr Asn Thr Thr Ser Glu
 385 390 395 400
 Ser Ile Thr Thr Pro Pro Leu Val Gly Glu Val Ile Phe Ser Glu Asn
 405 410 415
 Thr Ala Lys Gly His Gly Gly Gly Ile Cys Thr Asn Lys Leu Ser Leu
 420 425 430
 Ser Asn Leu Lys Thr Val Thr Leu Thr Lys Asn Ser Ala Lys Glu Ser
 435 440 445
 Gly Gly Ala Ile Phe Thr Asp Leu Ala Ser Ile Pro Thr Thr Asp Thr
 450 455 460
 Pro Glu Ser Ser Thr Pro Ser Ser Ser Ser Pro Ala Ser Thr Pro Glu
 465 470 475 480
 Val Val Ala Ser Ala Lys Ile Asn Arg Phe Phe Ala Ser Thr Ala Glu
 485 490 495
 Pro Ala Ala Pro Ser Leu Thr Glu Ala Glu Ser Asp Gln Thr Asp Gln
 500 505 510
 Thr Glu Thr Ser Asp Thr Asn Ser Asp Ile Asp Val Ser Ile Glu Asn
 515 520 525
 Ile Leu Asn Val Ala Ile Asn Gln Asn Thr Ser Ala Lys Lys Gly Gly
 530 535 540
 Ala Ile Tyr Gly Lys Lys Ala Lys Leu Ser Arg Ile Asn Asn Leu Glu
 545 550 555 560
 Leu Ser Gly Asn Ser Ser Gln Asp Val Gly Gly Leu Cys Leu Thr
 565 570 575
 Glu Ser Val Glu Phe Asp Ala Ile Gly Ser Leu Leu Ser His Tyr Asn
 580 585 590
 Ser Ala Ala Lys Glu Gly Gly Val Ile His Ser Lys Thr Val Thr Leu
 595 600 605
 Ser Asn Leu Lys Ser Thr Phe Thr Phe Ala Asp Asn Thr Val Lys Ala
 610 615 620
 Ile Val Glu Ser Thr Pro Glu Ala Pro Glu Glu Ile Pro Pro Val Glu
 625 630 635 640
 Gly Glu Glu Ser Thr Ala Thr Glu Asn Pro Asn Ser Asn Thr Glu Gly
 645 650 655
 Ser Ser Ala Asn Thr Asn Leu Glu Gly Ser Gln Gly Asp Thr Ala Asp
 660 665 670
 Thr Gly Thr Gly Val Val Asn Asn Glu Ser Gln Asp Thr Ser Asp Thr
 675 680 685
 Gly Asn Ala Glu Ser Gly Glu Gln Leu Gln Asp Ser Thr Gln Ser Asn
 690 695 700
 Glu Glu Asn Thr Leu Pro Asn Ser Ser Ile Asp Gln Ser Asn Glu Asn
 705 710 715 720
 Thr Asp Glu Ser Ser Asp Ser His Thr Glu Glu Ile Thr Asp Glu Ser
 725 730 735
 Val Ser Ser Ser Ser Lys Ser Gly Ser Ser Thr Pro Gln Asp Gly Gly
 740 745 750
 Ala Ala Ser Ser Gly Ala Pro Ser Gly Asp Gln Ser Ile Ser Ala Asn
 755 760 765
 Ala Cys Leu Ala Lys Ser Tyr Ala Ala Ser Thr Asp Ser Ser Pro Val

770	775	780
Ser Asn Ser Ser Gly Ser Asp Val Thr Ala Ser Ser Asp Asn Pro Asp		
785	790	795
Ser Ser Ser Ser Gly Asp Ser Ala Gly Asp Ser Glu Gly Pro Thr Glu		800
	805	810
Pro Glu Ala Gly Ser Thr Thr Glu Thr Pro Thr Leu Ile Gly Gly Gly		815
	820	825
Ala Ile Tyr Gly Glu Thr Val Lys Ile Glu Asn Phe Ser Gly Gln Gly		830
	835	840
Ile Phe Ser Gly Asn Lys Ala Ile Asp Asn Thr Thr Glu Gly Ser Ser		845
	850	855
Ser Lys Ser Asn Val Leu Gly Gly Ala Val Tyr Ala Lys Thr Leu Phe		860
	865	870
Asn Leu Asp Ser Gly Ser Ser Arg Arg Thr Val Thr Phe Ser Gly Asn		875
	885	890
Thr Val Ser Ser Gln Ser Thr Thr Gly Gln Val Ala Gly Gly Ala Ile		895
	900	905
Tyr Ser Pro Thr Val Thr Ile Ala Thr Pro Val Val Phe Ser Lys Asn		910
	915	920
Ser Ala Thr Asn Asn Ala Asn Asn Ala Thr Asp Thr Gln Arg Lys Asp		925
	930	935
Thr Phe Gly Gly Ala Ile Gly Ala Thr Ser Ala Val Ser Leu Ser Gly		940
	945	950
Gly Ala His Phe Leu Glu Asn Val Ala Asp Leu Gly Ser Ala Ile Gly		955
	965	970
Leu Val Pro Asp Thr Gln Asn Thr Glu Thr Val Lys Leu Glu Ser Gly		975
	980	985
Ser Tyr Tyr Phe Glu Lys Asn Lys Ala Leu Lys Arg Ala Thr Ile Tyr		990
	995	1000
Ala Pro Val Val Ser Ile Lys Ala Tyr Thr Ala Thr Phe Asn Gln Asn		1005
	1010	1015
Arg Ser Leu Glu Glu Gly Ser Ala Ile Tyr Phe Thr Lys Glu Ala Ser		1020
	1025	1030
Ile Glu Ser Leu Gly Ser Val Leu Phe Thr Gly Asn Leu Val Thr Pro		1035
	1045	1050
Thr Leu Ser Thr Thr Thr Glu Gly Thr Pro Ala Thr Thr Ser Gly Asp		1055
	1060	1065
Val Thr Lys Tyr Gly Ala Ala Ile Phe Gly Gln Ile Ala Ser Ser Asn		1070
	1075	1080
Gly Ser Gln Thr Asp Asn Leu Pro Leu Lys Leu Ile Ala Ser Gly Gly		1085
	1090	1095
Asn Ile Cys Phe Arg Asn Asn Glu Tyr Arg Pro Thr Ser Ser Asp Thr		1100
	1105	1110
Gly Thr Ser Thr Phe Cys Ser Ile Ala Gly Asp Val Lys Leu Thr Met		1115
	1125	1130
Gln Ala Ala Lys Gly Lys Thr Ile Ser Phe Phe Asp Ala Ile Arg Thr		1135
	1140	1145
Ser Thr Lys Lys Thr Gly Thr Gln Ala Thr Ala Tyr Asp Thr Leu Asp		1150
	1155	1160
Ile Asn Lys Ser Glu Asp Ser Glu Thr Val Asn Ser Ala Phe Thr Gly		1165
	1170	1175
Thr Ile Leu Phe Ser Ser Glu Leu His Glu Asn Lys Ser Tyr Ile Pro		1180
	1185	1190
Gln Asn Val Val Leu His Ser Gly Ser Leu Val Leu Lys Pro Asn Thr		1195
	1205	1210
Glu Leu His Val Ile Ser Phe Glu Gln Lys Glu Gly Ser Ser Leu Val		1215
	1220	1225
Met Thr Pro Gly Ser Val Leu Ser Asn Gln Thr Val Ala Asp Gly Ala		1230

1235 1240 1245
 Leu Val Ile Asn Asn Met Thr Ile Asp Leu Ser Ser Val Glu Lys Asn
 1250 1255 1260
 Gly Ile Ala Glu Gly Asn Ile Phe Thr Pro Pro Glu Leu Arg Ile Ile
 1265 1270 1275 1280
 Asp Thr Thr Thr Ser Gly Ser Gly Gly Thr Pro Ser Thr Asp Ser Glu
 1285 1290 1295
 Ser Asn Gln Asn Ser Asp Asp Thr Lys Glu Gln Asn Asn Asn Asp Ala
 1300 1305 1310
 Ser Asn Gln Gly Glu Ser Ala Asn Gly Ser Ser Ser Pro Ala Val Ala
 1315 1320 1325
 Ala Ala His Thr Ser Arg Thr Arg Asn Phe Ala Ala Ala Thr Ala
 1330 1335 1340
 Thr Pro Thr Thr Thr Pro Thr Ala Thr Thr Thr Thr Ser Asn Gln Val
 1345 1350 1355 1360
 Ile Leu Gly Gly Glu Ile Lys Leu Ile Asp Pro Asn Gly Thr Phe Phe
 1365 1370 1375
 Gln Asn Pro Ala Leu Arg Ser Asp Gln Gln Ile Ser Leu Leu Val Leu
 1380 1385 1390
 Pro Thr Asp Ser Ser Lys Met Gln Ala Gln Lys Ile Val Leu Thr Gly
 1395 1400 1405
 Asp Ile Ala Pro Gln Lys Gly Tyr Thr Gly Thr Leu Thr Leu Asp Pro
 1410 1415 1420
 Asp Gln Leu Gln Asn Gly Thr Ile Ser Ala Leu Trp Lys Phe Asp Ser
 1425 1430 1435 1440
 Tyr Arg Gln Trp Ala Tyr Val Pro Arg Asp Asn His Phe Tyr Ala Asn
 1445 1450 1455
 Ser Ile Leu Gly Ser Gln Met Ser Met Val Thr Val Lys Gln Gly Leu
 1460 1465 1470
 Leu Asn Asp Lys Met Asn Leu Ala Arg Phe Asp Glu Val Ser Tyr Asn
 1475 1480 1485
 Asn Leu Trp Ile Ser Gly Leu Gly Thr Met Leu Ser Gln Val Gly Thr
 1490 1495 1500
 Pro Thr Ser Glu Glu Phe Thr Tyr Tyr Ser Arg Gly Ala Ser Val Ala
 1505 1510 1515 1520
 Leu Asp Ala Lys Pro Ala His Asp Val Ile Val Gly Ala Ala Phe Ser
 1525 1530 1535
 Lys Met Ile Gly Lys Thr Lys Ser Leu Lys Arg Glu Asn Asn Tyr Thr
 1540 1545 1550
 His Lys Gly Ser Glu Tyr Ser Tyr Gln Ala Ser Val Tyr Gly Gly Lys
 1555 1560 1565
 Pro Phe His Phe Val Ile Asn Lys Lys Thr Glu Lys Ser Leu Pro Leu
 1570 1575 1580
 Leu Leu Gln Gly Val Ile Ser Tyr Gly Tyr Ile Lys His Asp Thr Val
 1585 1590 1595 1600
 Thr His Tyr Pro Thr Ile Arg Glu Arg Asn Gln Gly Glu Trp Glu Asp
 1605 1610 1615
 Leu Gly Trp Leu Thr Ala Leu Arg Val Ser Ser Val Leu Arg Thr Pro
 1620 1625 1630
 Ala Gln Gly Asp Thr Lys Arg Ile Thr Val Tyr Gly Glu Leu Glu Tyr
 1635 1640 1645
 Ser Ser Ile Arg Gln Lys Gln Phe Thr Glu Thr Glu Tyr Asp Pro Arg
 1650 1655 1660
 Tyr Phe Asp Asn Cys Thr Tyr Arg Asn Leu Ala Ile Pro Met Gly Leu
 1665 1670 1675 1680
 Ala Phe Glu Gly Glu Leu Ser Gly Asn Asp Ile Leu Met Tyr Asn Arg
 1685 1690 1695
 Phe Ser Val Ala Tyr Met Pro Ser Ile Tyr Arg Asn Ser Pro Thr Cys

1700 1705 1710
 Lys Tyr Gln Val Leu Ser Ser Gly Glu Gly Glu Ile Ile Cys Gly
 1715 1720 1725
 Val Pro Thr Arg Asn Ser Ala Arg Gly Glu Tyr Ser Thr Gln Leu Tyr
 1730 1735 1740
 Pro Gly Pro Leu Trp Thr Leu Tyr Gly Ser Tyr Thr Ile Glu Ala Asp
 1745 1750 1755 1760
 Ala His Thr Leu Ala His Met Met Asn Cys Gly Ala Arg Met Thr Phe
 1765 1770 1775

<210> 180

<211> 1752

<212> PRT

<213> Chlamydia

<400> 180

Met Lys Trp Leu Ser Ala Thr Ala Val Phe Ala Ala Val Leu Pro Ser
 1 5 10 15
 Val Ser Gly Phe Cys Phe Pro Glu Pro Lys Glu Leu Asn Phe Ser Arg
 20 25 30
 Val Glu Thr Ser Ser Ser Thr Thr Phe Thr Glu Thr Ile Gly Glu Ala
 35 40 45
 Gly Ala Glu Tyr Ile Val Ser Gly Asn Ala Ser Phe Thr Lys Phe Thr
 50 55 60
 Asn Ile Pro Thr Thr Asp Thr Thr Thr Pro Thr Asn Ser Asn Ser Ser
 65 70 75 80
 Ser Ser Ser Gly Glu Thr Ala Ser Val Ser Glu Asp Ser Asp Ser Thr
 85 90 95
 Thr Thr Thr Pro Asp Pro Lys Gly Gly Glu Ala Phe Tyr Asn Ala His
 100 105 110
 Ser Gly Val Leu Ser Phe Met Thr Arg Ser Gly Thr Glu Gly Ser Leu
 115 120 125
 Thr Leu Ser Glu Ile Lys Met Thr Gly Glu Gly Gly Ala Ile Phe Ser
 130 135 140
 Gln Gly Glu Leu Leu Phe Thr Asp Leu Thr Ser Leu Thr Ile Gln Asn
 145 150 155 160
 Asn Leu Ser Gln Leu Ser Gly Gly Ala Ile Phe Gly Gly Ser Thr Ile
 165 170 175
 Ser Leu Ser Gly Ile Thr Lys Ala Thr Phe Ser Cys Asn Ser Ala Glu
 180 185 190
 Val Pro Ala Pro Val Lys Lys Pro Thr Glu Pro Lys Ala Gln Thr Ala
 195 200 205
 Ser Glu Thr Ser Gly Ser Ser Ser Ser Ser Gly Asn Asp Ser Val Ser
 210 215 220
 Ser Pro Ser Ser Ser Arg Ala Glu Pro Ala Ala Ala Asn Leu Gln Ser
 225 230 235 240
 His Phe Ile Cys Ala Thr Ala Thr Pro Ala Ala Gln Thr Asp Thr Glu
 245 250 255
 Thr Ser Thr Pro Ser His Lys Pro Gly Ser Gly Gly Ala Ile Tyr Ala
 260 265 270
 Lys Gly Asp Leu Thr Ile Ala Asp Ser Gln Glu Val Leu Phe Ser Ile
 275 280 285
 Asn Lys Ala Thr Lys Asp Gly Gly Ala Ile Phe Ala Glu Lys Asp Val
 290 295 300
 Ser Phe Glu Asn Ile Thr Ser Leu Lys Val Gln Thr Asn Gly Ala Glu
 305 310 315 320
 Glu Lys Gly Gly Ala Ile Tyr Ala Lys Gly Asp Leu Ser Ile Gln Ser
 325 330 335

Ser Lys Gln Ser Leu Phe Asn Ser Asn Tyr Ser Lys Gln Gly Gly Gly
 340 345 350
 Ala Leu Tyr Val Glu Gly Gly Ile Asn Phe Gln Asp Leu Glu Gly Ile
 355 360 365
 Arg Ile Lys Tyr Asn Lys Ala Gly Thr Phe Glu Thr Lys Lys Ile Thr
 370 375 380
 Leu Pro Ser Leu Lys Ala Gln Ala Ser Ala Gly Asn Ala Asp Ala Trp
 385 390 395 400
 Ala Ser Ser Ser Pro Gln Ser Gly Ser Gly Ala Thr Thr Val Ser Asp
 405 410 415
 Ser Gly Asp Ser Ser Ser Gly Ser Asp Ser Asp Thr Ser Glu Thr Val
 420 425 430
 Pro Val Thr Ala Lys Gly Gly Gly Leu Tyr Thr Asp Lys Asn Leu Ser
 435 440 445
 Ile Thr Asn Ile Thr Gly Ile Ile Glu Ile Ala Asn Asn Lys Ala Thr
 450 455 460
 Asp Val Gly Gly Gly Ala Tyr Val Lys Gly Thr Leu Thr Cys Glu Asn
 465 470 475 480
 Ser His Arg Leu Gln Phe Leu Lys Asn Ser Ser Asp Lys Gln Gly Gly
 485 490 495
 Gly Ile Tyr Gly Glu Asp Asn Ile Thr Leu Ser Asn Leu Thr Gly Lys
 500 505 510
 Thr Leu Phe Gln Glu Asn Thr Ala Lys Glu Glu Gly Gly Leu Phe
 515 520 525
 Ile Lys Gly Thr Asp Lys Ala Leu Thr Met Thr Gly Leu Asp Ser Phe
 530 535 540
 Cys Leu Ile Asn Asn Thr Ser Glu Lys His Gly Gly Ala Phe Val
 545 550 555 560
 Thr Lys Glu Ile Ser Gln Thr Tyr Thr Ser Asp Val Glu Thr Ile Pro
 565 570 575
 Gly Ile Thr Pro Val His Gly Glu Thr Val Ile Thr Gly Asn Lys Ser
 580 585 590
 Thr Gly Gly Asn Gly Gly Gly Val Cys Thr Lys Arg Leu Ala Leu Ser
 595 600 605
 Asn Leu Gln Ser Ile Ser Ile Ser Gly Asn Ser Ala Ala Glu Asn Gly
 610 615 620
 Gly Gly Ala His Thr Cys Pro Asp Ser Phe Pro Thr Ala Asp Thr Ala
 625 630 635 640
 Glu Gln Pro Ala Ala Ala Ser Ala Ala Thr Ser Thr Pro Lys Ser Ala
 645 650 655
 Pro Val Ser Thr Ala Leu Ser Thr Pro Ser Ser Ser Thr Val Ser Ser
 660 665 670
 Leu Thr Leu Leu Ala Ala Ser Ser Gln Ala Ser Pro Ala Thr Ser Asn
 675 680 685
 Lys Glu Thr Gln Asp Pro Asn Ala Asp Thr Asp Leu Leu Ile Asp Tyr
 690 695 700
 Val Val Asp Thr Thr Ile Ser Lys Asn Thr Ala Lys Lys Gly Gly Gly
 705 710 715 720
 Ile Tyr Ala Lys Lys Ala Lys Met Ser Arg Ile Asp Gln Leu Asn Ile
 725 730 735
 Ser Glu Asn Ser Ala Thr Glu Ile Gly Gly Gly Ile Cys Lys Glu
 740 745 750
 Ser Leu Glu Leu Asp Ala Leu Val Ser Leu Ser Val Thr Glu Asn Leu
 755 760 765
 Val Gly Lys Glu Gly Gly Glu Leu His Ala Lys Thr Val Asn Ile Ser
 770 775 780
 Asn Leu Lys Ser Gly Phe Ser Phe Ser Asn Asn Lys Ala Asn Ser Ser
 785 790 795 800

Ser Thr Gly Val Ala Thr Thr Ala Ser Ala Pro Ala Ala Ala Ala Ala
 805 810 815
 Ser Leu Gln Ala Ala Ala Ala Ala Pro Ser Ser Pro Ala Thr Pro
 820 825 830
 Thr Tyr Ser Gly Val Val Gly Gly Ala Ile Tyr Gly Glu Lys Val Thr
 835 840 845
 Phe Ser Gln Cys Ser Gly Thr Cys Gln Phe Ser Gly Asn Gln Ala Ile
 850 855 860
 Asp Asn Asn Pro Ser Gln Ser Ser Leu Asn Val Gln Gly Gly Ala Ile
 865 870 875 880
 Tyr Ala Lys Thr Ser Leu Ser Ile Gly Ser Ser Asp Ala Gly Thr Ser
 885 890 895
 Tyr Ile Phe Ser Gly Asn Ser Val Ser Thr Gly Lys Ser Gln Thr Thr
 900 905 910
 Gly Gln Ile Ala Gly Gly Ala Ile Tyr Ser Pro Thr Val Thr Leu Asn
 915 920 925
 Cys Pro Ala Thr Phe Ser Asn Asn Thr Ala Ser Ile Ala Thr Pro Lys
 930 935 940
 Thr Ser Ser Glu Asp Gly Ser Ser Gly Asn Ser Ile Lys Asp Thr Ile
 945 950 955 960
 Gly Gly Ala Ile Ala Gly Thr Ala Ile Thr Leu Ser Gly Val Ser Arg
 965 970 975
 Phe Ser Gly Asn Thr Ala Asp Leu Gly Ala Ala Ile Gly Thr Leu Ala
 980 985 990
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<212> DNA

<213> Chlamydia

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<213> Chlamydia

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<212> DNA

<213> Chlamydia

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<211> 2847

<212> DNA

<213> Chlamydia

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<211> 2466

<212> DNA

<213> Chlamydia

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<220>

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<223> Xaa = Any Amino Acid

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Lys Glu Lys Gly Asp Leu Ser Ile Gln Asn Phe Arg Phe Leu Ser Phe
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Phe Leu Ser Asn Ser Gly Asp Glu Asn Phe Tyr Glu Asn Val Glu Leu
              485              490              495
Leu Ser Lys Glu Gln Asn Asn Ile Pro Leu Leu Thr Leu Pro Lys Glu
              500              505              510
Gln Ser His Leu His Leu Pro Asp Gly Asn Leu Ser Ser His Phe Gly
              515              520              525
Tyr Gln Gly Asp Trp Thr Phe Ser Trp Lys Asp Ser Asp Glu Gly His
              530              535              540
Ser Leu Ile Ala Asn Trp Thr Pro Lys Asn Tyr Val Pro His Pro Glu
              545              550              555
Arg Gln Ser Thr Leu Val Ala Asn Thr Leu Trp Asn Thr Tyr Ser Asp
              560              565              570
Met Gln Ala Val Gln Ser Met Ile Asn Thr Thr Ala His Gly Gly Ala
              580              585              590
Tyr Leu Phe Gly Thr Trp Gly Ser Ala Val Ser Asn Leu Phe Tyr Val
              595              600              605
His Asp Ser Ser Gly Lys Pro Ile Asp Asn Trp His His Arg Ser Leu
              610              615              620
Gly Tyr Leu Phe Gly Ile Ser Thr His Ser Leu Asp Asp His Ser Phe
              625              630              635
Cys Leu Ala Ala Gly Gln Leu Leu Gly Lys Ser Ser Asp Ser Phe Ile
              640              645              650
Thr Ser Thr Glu Thr Thr Ser Tyr Ile Ala Thr Val Gln Ala Gln Leu
              655              660              665
Ala Thr Ser Leu Met Lys Ile Ser Ala Gln Ala Cys Tyr Asn Glu Ser
              670              675              680
Ile His Glu Leu Lys Thr Lys Tyr Arg Ser Phe Ser Lys Glu Gly Phe
              685              690              695
Gly Ser Trp His Ser Val Ala Val Ser Gly Glu Val Cys Ala Ser Ile
              700              705              710
Pro Ile Val Ser Asn Gly Ser Gly Leu Phe Ser Ser Phe Ser Ile Phe
              715              720              725
Ser Lys Leu Gln Gly Phe Ser Gly Thr Gln Asp Gly Phe Glu Glu Ser
              730              735              740
Ser Gly Glu Ile Arg Ser Phe Ser Ala Ser Ser Phe Arg Asn Ile Ser
              745              750              755
Leu Pro Ile Gly Ile Thr Phe Glu Lys Lys Ser Gln Lys Thr Arg Thr
              760              765              770
Tyr Tyr Tyr Phe Leu Gly Ala Tyr Ile Gln Asp Leu Lys Arg Asp Val
              775              780              785
Glu Ser Gly Pro Val Val Leu Leu Lys Asn Ala Val Ser Trp Asp Ala
              790              795              800
Pro Met Ala Asn Leu Asp Ser Arg Ala Tyr Met Phe Arg Leu Thr Asn
              805              810              815
Gln Arg Ala Leu His Arg Leu Gln Thr Leu Leu Asn Val Ser Cys Val
              820              825              830
Leu Arg Gly Gln Ser His Ser Tyr Ser Leu Asp Leu Gly Thr Thr Tyr
              835              840              845

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850
 Arg Phe
 865

 <210> 190
 <211> 1006
 <212> PRT
 <213> Chlamydia

 <400> 190
 Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Asp Ser Ser Leu
 1 5 10 15
 Val Pro His His His His His Met Ile Pro Gln Gly Ile Tyr Asp
 20 25 30
 Gly Glu Thr Leu Thr Val Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro
 35 40 45
 Ser Gly Thr Thr Val Phe Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu
 50 55 60
 Asp Asn Ser Ile Ala Ala Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu
 65 70 75 80
 Gly Ser Phe Thr Val Leu Gly Arg Gly His Ser Leu Thr Phe Glu Asn
 85 90 95
 Ile Arg Thr Ser Thr Asn Gly Ala Ala Leu Ser Asn Ser Ala Ala Asp
 100 105 110
 Gly Leu Phe Thr Ile Glu Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys
 115 120 125
 Asn Ser Leu Leu Ala Val Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser
 130 135 140
 Gln Thr Pro Thr Thr Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser
 145 150 155 160
 Lys Thr Asp Leu Leu Leu Leu Asn Asn Glu Lys Phe Ser Phe Tyr Ser
 165 170 175
 Asn Leu Val Ser Gly Asp Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr
 180 185 190
 Val Gln Gly Ile Ser Lys Leu Cys Val Phe Gln Glu Asn Thr Ala Gln
 195 200 205
 Ala Asp Gly Gly Ala Cys Gln Val Val Thr Ser Phe Ser Ala Met Ala
 210 215 220
 Asn Glu Ala Pro Ile Ala Phe Val Ala Asn Val Ala Gly Val Arg Gly
 225 230 235 240
 Gly Gly Ile Ala Ala Val Gln Asp Gly Gln Gln Gly Val Ser Ser Ser
 245 250 255
 Thr Ser Thr Glu Asp Pro Val Val Ser Phe Ser Arg Asn Thr Ala Val
 260 265 270
 Glu Phe Asp Gly Asn Val Ala Arg Val Gly Gly Ile Tyr Ser Tyr
 275 280 285
 Gly Asn Val Ala Phe Leu Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn
 290 295 300
 Val Ala Ser Pro Val Tyr Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln
 305 310 315 320
 Ala Ser Asn Thr Ser Asn Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys
 325 330 335
 Lys Asn Gly Ala Gln Ala Gly Ser Asn Asn Ser Gly Ser Val Ser Phe
 340 345 350
 Asp Gly Glu Gly Val Val Phe Phe Ser Ser Asn Val Ala Ala Gly Lys
 355 360 365
 Gly Gly Ala Ile Tyr Ala Lys Lys Leu Ser Val Ala Asn Cys Gly Pro
 370 375 380

Val Gln Phe Leu Arg Asn Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu
 385 390 395 400
 Gly Glu Ser Gly Glu Leu Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile
 405 410 415
 Phe Asp Gly Asn Leu Lys Arg Thr Ala Lys Glu Asn Ala Ala Asp Val
 420 425 430
 Asn Gly Val Thr Val Ser Ser Gln Ala Ile Ser Met Gly Ser Gly Gly
 435 440 445
 Lys Ile Thr Thr Leu Arg Ala Lys Ala Gly His Gln Ile Leu Phe Asn
 450 455 460
 Asp Pro Ile Glu Met Ala Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser
 465 470 475 480
 Lys Leu Leu Lys Ile Asn Asp Gly Glu Gly Tyr Thr Gly Asp Ile Val
 485 490 495
 Phe Ala Asn Gly Ser Ser Thr Leu Tyr Gln Asn Val Thr Ile Glu Gln
 500 505 510
 Gly Arg Ile Val Leu Arg Glu Lys Ala Lys Leu Ser Val Asn Ser Leu
 515 520 525
 Ser Gln Thr Gly Gly Ser Leu Tyr Met Glu Ala Gly Ser Thr Leu Asp
 530 535 540
 Phe Val Thr Pro Gln Pro Pro Gln Gln Pro Pro Ala Ala Asn Gln Leu
 545 550 555 560
 Ile Thr Leu Ser Asn Leu His Leu Ser Leu Ser Ser Leu Leu Ala Asn
 565 570 575
 Asn Ala Val Thr Asn Pro Pro Thr Asn Pro Pro Ala Gln Asp Ser His
 580 585 590
 Pro Ala Val Ile Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly
 595 600 605
 Pro Ile Phe Phe Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp
 610 615 620
 Trp Leu Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu Gly
 625 630 635 640
 Thr Lys Pro Pro Ala Asn Ala Pro Ser Asp Leu Thr Leu Gly Asn Glu
 645 650 655
 Met Pro Lys Tyr Gly Tyr Gln Gly Ser Trp Lys Leu Ala Trp Asp Pro
 660 665 670
 Asn Thr Ala Asn Asn Gly Pro Tyr Thr Leu Lys Ala Thr Trp Thr Lys
 675 680 685
 Thr Gly Tyr Asn Pro Gly Pro Glu Arg Val Ala Ser Leu Val Pro Asn
 690 695 700
 Ser Leu Trp Gly Ser Ile Leu Asp Ile Arg Ser Ala His Ser Ala Ile
 705 710 715 720
 Gln Ala Ser Val Asp Gly Arg Ser Tyr Cys Arg Gly Leu Trp Val Ser
 725 730 735
 Gly Val Ser Asn Phe Phe Tyr His Asp Arg Asp Ala Leu Gly Gln Gly
 740 745 750
 Tyr Arg Tyr Ile Ser Gly Gly Tyr Ser Leu Gly Ala Asn Ser Tyr Phe
 755 760 765
 Gly Ser Ser Met Phe Gly Leu Ala Phe Thr Glu Val Phe Gly Arg Ser
 770 775 780
 Lys Asp Tyr Val Val Cys Arg Ser Asn His His Ala Cys Ile Gly Ser
 785 790 795 800
 Val Tyr Leu Ser Thr Gln Gln Ala Leu Cys Gly Ser Tyr Leu Phe Gly
 805 810 815
 Asp Ala Phe Ile Arg Ala Ser Tyr Gly Phe Gly Asn Gln His Met Lys
 820 825 830
 Thr Ser Tyr Thr Phe Ala Glu Glu Ser Asp Val Arg Trp Asp Asn Asn
 835 840 845

Cys Leu Ala Gly Glu Ile Gly Ala Gly Leu Pro Ile Val Ile Thr Pro
 850 855 860
 Ser Lys Leu Tyr Leu Asn Glu Leu Arg Pro Phe Val Gln Ala Glu Phe
 865 870 875 880
 Ser Tyr Ala Asp His Glu Ser Phe Thr Glu Gly Asp Gln Ala Arg
 885 890 895
 Ala Phe Lys Ser Ser Gly His Leu Leu Asn Leu Ser Val Pro Val Gly Val
 900 905 910
 Lys Phe Asp Arg Cys Ser Ser Thr His Pro Asn Lys Tyr Ser Phe Met
 915 920 925
 Ala Ala Tyr Ile Cys Asp Ala Tyr Arg Thr Ile Ser Gly Thr Glu Thr
 930 935 940
 Thr Leu Leu Ser His Gln Glu Thr Trp Thr Thr Asp Ala Phe His Leu
 945 950 955 960
 Ala Arg His Gly Val Val Val Arg Gly Ser Met Tyr Ala Ser Leu Thr
 965 970 975
 Ser Asn Ile Glu Val Tyr Gly His Gly Arg Tyr Glu Tyr Arg Asp Ala
 980 985 990
 Ser Arg Gly Tyr Gly Leu Ser Ala Gly Ser Lys Val Arg Phe
 995 1000 1005

<210> 191

<211> 977

<212> PRT

<213> Chlamydia

<400> 191

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Asp Ser Ser Leu
 1 5 10 15
 Val Pro Ser Ser Asp Pro His His His His His His Gly Leu Ala Arg
 20 25 30
 Glu Val Pro Ser Arg Ile Phe Leu Met Pro Asn Ser Val Pro Asp Pro
 35 40 45
 Thr Lys Glu Ser Leu Ser Asn Lys Ile Ser Leu Thr Gly Asp Thr His
 50 55 60
 Asn Leu Thr Asn Cys Tyr Leu Asp Asn Leu Arg Tyr Ile Leu Ala Ile
 65 70 75 80
 Leu Gln Lys Thr Pro Asn Glu Gly Ala Ala Val Thr Ile Thr Asp Tyr
 85 90 95
 Leu Ser Phe Phe Asp Thr Gln Lys Glu Gly Ile Tyr Phe Ala Lys Asn
 100 105 110
 Leu Thr Pro Glu Ser Gly Gly Ala Ile Gly Tyr Ala Ser Pro Asn Ser
 115 120 125
 Pro Thr Val Glu Ile Arg Asp Thr Ile Gly Pro Val Ile Phe Glu Asn
 130 135 140
 Asn Thr Cys Cys Arg Leu Phe Thr Trp Arg Asn Pro Tyr Ala Ala Asp
 145 150 155 160
 Lys Ile Arg Glu Gly Gly Ala Ile His Ala Gln Asn Leu Tyr Ile Asn
 165 170 175
 His Asn His Asp Val Val Gly Phe Met Lys Asn Phe Ser Tyr Val Gln
 180 185 190
 Gly Gly Ala Ile Ser Thr Ala Asn Thr Phe Val Val Ser Glu Asn Gln
 195 200 205
 Ser Cys Phe Leu Phe Met Asp Asn Ile Cys Ile Gln Thr Asn Thr Ala
 210 215 220
 Gly Lys Gly Gly Ala Ile Tyr Ala Gly Thr Ser Asn Ser Phe Glu Ser
 225 230 235 240
 Asn Asn Cys Asp Leu Phe Phe Ile Asn Asn Ala Cys Cys Ala Gly Gly

245 250 255
 Ala Ile Phe Ser Pro Ile Cys Ser Leu Thr Gly Asn Arg Gly Asn Ile
 260 265 270
 Val Phe Tyr Asn Asn Arg Cys Phe Lys Asn Val Glu Thr Ala Ser Ser
 275 280 285
 Glu Ala Ser Asp Gly Gly Ala Ile Lys Val Thr Thr Arg Leu Asp Val
 290 295 300
 Thr Gly Asn Arg Gly Arg Ile Phe Phe Ser Asp Asn Ile Thr Lys Asn
 305 310 315 320
 Tyr Gly Gly Ala Ile Tyr Ala Pro Val Val Thr Leu Val Asp Asn Gly
 325 330 335
 Pro Thr Tyr Phe Ile Asn Asn Ile Ala Asn Asn Lys Gly Gly Ala Ile
 340 345 350
 Tyr Ile Asp Gly Thr Ser Asn Ser Lys Ile Ser Ala Asp Arg His Ala
 355 360 365
 Ile Ile Phe Asn Glu Asn Ile Val Thr Asn Val Thr Asn Ala Asn Gly
 370 375 380
 Thr Ser Thr Ser Ala Asn Pro Pro Arg Arg Asn Ala Ile Thr Val Ala
 385 390 395 400
 Ser Ser Ser Gly Glu Ile Leu Leu Gly Ala Gly Ser Ser Gln Asn Leu
 405 410 415
 Ile Phe Tyr Asp Pro Ile Glu Val Ser Asn Ala Gly Val Ser Val Ser
 420 425 430
 Phe Asn Lys Glu Ala Asp Gln Thr Gly Ser Val Val Phe Ser Gly Ala
 435 440 445
 Thr Val Asn Ser Ala Asp Phe His Gln Arg Asn Leu Gln Thr Lys Thr
 450 455 460
 Pro Ala Pro Leu Thr Leu Ser Asn Gly Phe Leu Cys Ile Glu Asp His
 465 470 475 480
 Ala Gln Leu Thr Val Asn Arg Phe Thr Gln Thr Gly Gly Val Val Ser
 485 490 495
 Leu Gly Asn Gly Ala Val Leu Ser Cys Tyr Lys Asn Gly Thr Gly Asp
 500 505 510
 Ser Ala Ser Asn Ala Ser Ile Thr Leu Lys His Ile Gly Leu Asn Leu
 515 520 525
 Ser Ser Ile Leu Lys Ser Gly Ala Glu Ile Pro Leu Leu Trp Val Glu
 530 535 540
 Pro Thr Asn Asn Ser Asn Asn Tyr Thr Ala Asp Thr Ala Ala Thr Phe
 545 550 555 560
 Ser Leu Ser Asp Val Lys Leu Ser Leu Ile Asp Asp Tyr Gly Asn Ser
 565 570 575
 Pro Tyr Glu Ser Thr Asp Leu Thr His Ala Leu Ser Ser Gln Pro Met
 580 585 590
 Leu Ser Ile Ser Glu Ala Ser Asp Asn Gln Leu Gln Ser Glu Asn Ile
 595 600 605
 Asp Phe Ser Gly Leu Asn Val Pro His Tyr Gly Trp Gln Gly Leu Trp
 610 615 620
 Thr Trp Gly Trp Ala Lys Thr Gln Asp Pro Glu Pro Ala Ser Ser Ala
 625 630 635 640
 Thr Ile Thr Asp Pro Gln Lys Ala Asn Arg Phe His Arg Thr Leu Leu
 645 650 655
 Leu Thr Trp Leu Pro Ala Gly Tyr Val Pro Ser Pro Lys His Arg Ser
 660 665 670
 Pro Leu Ile Ala Asn Thr Leu Trp Gly Asn Met Leu Leu Ala Thr Glu
 675 680 685
 Ser Leu Lys Asn Ser Ala Glu Leu Thr Pro Ser Gly His Pro Phe Trp
 690 695 700
 Gly Ile Thr Gly Gly Gly Leu Gly Met Met Val Tyr Gln Asp Pro Arg

[illegible]

Asn Phe Ser Asp Ile Tyr Gly Gly Ala Ile Phe Thr Gly Ser Leu Arg
 130 135 140
 Glu Glu Asp Lys Leu Asp Gly Gln Ile Pro Glu Val Leu Ile Ser Gly
 145 150 155 160
 Asn Ala Gly Asp Val Val Phe Ser Gly Asn Ser Ser Lys Arg Asp Glu
 165 170 175
 His Leu Pro His Thr Gly Gly Gly Ala Ile Cys Thr Gln Asn Leu Thr
 180 185 190
 Ile Ser Gln Asn Thr Gly Asn Val Leu Phe Tyr Asn Asn Val Ala Cys
 195 200 205
 Ser Gly Gly Ala Val Arg Ile Glu Asp His Gly Asn Val Leu Leu Glu
 210 215 220
 Ala Phe Gly Gly Asp Ile Val Phe Lys Gly Asn Ser Ser Phe Arg Ala
 225 230 235 240
 Gln Gly Ser Asp Ala Ile Tyr Phe Ala Gly Lys Glu Ser His Ile Thr
 245 250 255
 Ala Leu Asn Ala Thr Glu Gly His Ala Ile Val Phe His Asp Ala Leu
 260 265 270
 Val Phe Glu Asn Leu Lys Glu Arg Lys Ser Ala Glu Val Leu Leu Ile
 275 280 285
 Asn Ser Arg Glu Asn Pro Gly Tyr Thr Gly Ser Ile Arg Phe Leu Glu
 290 295 300
 Ala Glu Ser Lys Val Pro Gln Cys Ile His Val Gln Gln Gly Ser Leu
 305 310 315 320
 Glu Leu Leu Asn Gly Ala Thr Leu Cys Ser Tyr Gly Phe Lys Gln Asp
 325 330 335
 Ala Gly Ala Lys Leu Val Leu Ala Ala Gly Ser Lys Leu Lys Ile Leu
 340 345 350
 Asp Ser Gly Thr Pro Val Gln Gly His Ala Ile Ser Lys Pro Glu Ala
 355 360 365
 Glu Ile Glu Ser Ser Ser Glu Pro Glu Gly Ala His Ser Leu Trp Ile
 370 375 380
 Ala Lys Asn Ala Gln Thr Thr Val Pro Met Val Asp Ile His Thr Ile
 385 390 395 400
 Ser Val Asp Leu Ala Ser Phe Ser Ser Ser Gln Gln Glu Gly Thr Val
 405 410 415
 Glu Ala Pro Gln Val Ile Val Pro Gly Gly Ser Tyr Val Arg Ser Gly
 420 425 430
 Glu Leu Asn Leu Glu Leu Val Asn Thr Thr Gly Thr Gly Tyr Glu Asn
 435 440 445
 His Ala Leu Leu Lys Asn Glu Ala Lys Val Pro Leu Met Ser Phe Val
 450 455 460
 Ala Ser Ser Asp Glu Ala Ser Ala Glu Ile Ser Asn Leu Ser Val Ser
 465 470 475 480
 Asp Leu Gln Ile His Val Ala Thr Pro Glu Ile Glu Glu Asp Thr Tyr
 485 490 495
 Gly His Met Gly Asp Trp Ser Glu Ala Lys Ile Gln Asp Gly Thr Leu
 500 505 510
 Val Ile Asn Trp Asn Pro Thr Gly Tyr Arg Leu Asp Pro Gln Lys Ala
 515 520 525
 Gly Ala Leu Val Phe Asn Ala Leu Trp Glu Glu Gly Ala Val Leu Ser
 530 535 540
 Ala Leu Lys Asn Ala Arg Phe Ala His Asn Leu Thr Ala Gln Arg Met
 545 550 555 560
 Glu Phe Asp Tyr Ser Thr Asn Val Trp Gly Phe Ala Phe Gly Gly Phe
 565 570 575
 Arg Thr Leu Ser Ala Glu Asn Leu Val Ala Ile Asp Gly Tyr Lys Gly
 580 585 590

Ala Tyr Gly Gly Ala Ser Ala Gly Val Asp Ile Gln Leu Met Glu Asp
 595 600 605
 Phe Val Leu Gly Val Ser Gly Ala Ala Phe Leu Gly Lys Met Asp Ser
 610 615 620
 Gln Lys Phe Asp Ala Glu Val Ser Arg Lys Gly Val Val Gly Ser Val
 625 630 635 640
 Tyr Thr Gly Phe Leu Ala Gly Ser Trp Phe Phe Lys Gly Gln Tyr Ser
 645 650 655
 Leu Gly Glu Thr Gln Asn Asp Met Lys Thr Arg Tyr Gly Val Leu Gly
 660 665 670
 Glu Ser Ser Ala Ser Trp Thr Ser Arg Gly Val Leu Ala Asp Ala Leu
 675 680 685
 Val Glu Tyr Arg Ser Leu Val Gly Pro Val Arg Pro Thr Phe Tyr Ala
 690 695 700
 Leu His Phe Asn Pro Tyr Val Glu Val Ser Tyr Ala Ser Met Lys Phe
 705 710 715 720
 Pro Gly Phe Thr Glu Gln Gly Arg Glu Ala Arg Ser Phe Glu Asp Ala
 725 730 735
 Ser Leu Thr Asn Ile Thr Ile Pro Leu Gly Met Lys Phe Glu Leu Ala
 740 745 750
 Phe Ile Lys Gly Gln Phe Ser Glu Val Asn Ser Leu Gly Ile Ser Tyr
 755 760 765
 Ala Trp Glu Ala Tyr Arg Lys Val Glu Gly Gly Ala Val Gln Leu Leu
 770 775 780
 Glu Ala Gly Phe Asp Trp Glu Gly Ala Pro Met Asp Leu Pro Arg Gln
 785 790 795 800
 Glu Leu Arg Val Ala Leu Glu Asn Asn Thr Glu Trp Ser Ser Tyr Phe
 805 810 815
 Ser Thr Val Leu Gly Leu Thr Ala Phe Cys Gly Gly Phe Thr Ser Thr
 820 825 830
 Asp Ser Lys Leu Gly Tyr Glu Ala Asn Thr Gly Leu Arg Leu Ile Phe
 835 840 845

<210> 193

<211> 778

<212> PRT

<213> Chlamydia

<400> 193

Met His His His His His His Gly Leu Ala Ser Cys Val Asp Leu His
 1 5 10 15
 Ala Gly Gly Gln Ser Val Asn Glu Leu Val Tyr Val Gly Pro Gln Ala
 20 25 30
 Val Leu Leu Leu Asp Gln Ile Arg Asp Leu Phe Val Gly Ser Lys Asp
 35 40 45
 Ser Gln Ala Glu Gly Gln Tyr Arg Leu Ile Val Gly Asp Pro Ser Ser
 50 55 60
 Phe Gln Glu Lys Asp Ala Asp Thr Leu Pro Gly Lys Val Glu Gln Ser
 65 70 75 80
 Thr Leu Phe Ser Val Thr Asn Pro Val Val Phe Gln Gly Val Asp Gln
 85 90 95
 Gln Asp Gln Val Ser Ser Gln Gly Leu Ile Cys Ser Phe Thr Ser Ser
 100 105 110
 Asn Leu Asp Ser Pro Arg Asp Gly Glu Ser Phe Leu Gly Ile Ala Phe
 115 120 125
 Val Gly Asp Ser Ser Lys Ala Gly Ile Thr Leu Thr Asp Val Lys Ala
 130 135 140
 Ser Leu Ser Gly Ala Ala Leu Tyr Ser Thr Glu Asp Leu Ile Phe Glu

145 150 155 160
 Lys Ile Lys Gly Gly Leu Glu Phe Ala Ser Cys Ser Ser Leu Glu Gln
 165 170 175
 Gly Gly Ala Cys Ala Ala Gln Ser Ile Leu Ile His Asp Cys Gln Gly
 180 185 190
 Leu Gln Val Lys His Cys Thr Thr Ala Val Asn Ala Glu Gly Ser Ser
 195 200 205
 Ala Asn Asp His Leu Gly Phe Gly Gly Gly Ala Phe Phe Val Thr Gly
 210 215 220
 Ser Leu Ser Gly Glu Lys Ser Leu Tyr Met Pro Ala Gly Asp Met Val
 225 230 235 240
 Val Ala Asn Cys Asp Gly Ala Ile Ser Phe Glu Gly Asn Ser Ala Asn
 245 250 255
 Phe Ala Asn Gly Gly Ala Ile Ala Ala Ser Gly Lys Val Leu Phe Val
 260 265 270
 Ala Asn Asp Lys Lys Thr Ser Phe Ile Glu Asn Arg Ala Leu Ser Gly
 275 280 285
 Gly Ala Ile Ala Ala Ser Ser Asp Ile Ala Phe Gln Asn Cys Ala Glu
 290 295 300
 Leu Val Phe Lys Gly Asn Cys Ala Ile Gly Thr Glu Asp Lys Gly Ser
 305 310 315 320
 Leu Gly Gly Gly Ala Ile Ser Ser Leu Gly Thr Val Leu Leu Gln Gly
 325 330 335
 Asn His Gly Ile Thr Cys Asp Lys Asn Glu Ser Ala Ser Gln Gly Gly
 340 345 350
 Ala Ile Phe Gly Lys Asn Cys Gln Ile Ser Asp Asn Glu Gly Pro Val
 355 360 365
 Val Phe Arg Asp Ser Thr Ala Cys Leu Gly Gly Gly Ala Ile Ala Ala
 370 375 380
 Gln Glu Ile Val Ser Ile Gln Asn Asn Gln Ala Gly Ile Ser Phe Glu
 385 390 395 400
 Gly Gly Lys Ala Ser Phe Gly Gly Gly Ile Ala Cys Gly Ser Phe Ser
 405 410 415
 Ser Ala Gly Gly Ala Ser Val Leu Gly Thr Ile Asp Ile Ser Lys Asn
 420 425 430
 Leu Gly Ala Ile Ser Phe Ser Arg Thr Leu Cys Thr Thr Ser Asp Leu
 435 440 445
 Gly Gln Met Glu Tyr Gln Gly Gly Ala Leu Phe Gly Glu Asn Ile
 450 455 460
 Ser Leu Ser Glu Asn Ala Gly Val Leu Thr Phe Lys Asp Asn Ile Val
 465 470 475 480
 Lys Thr Phe Ala Ser Asn Gly Lys Ile Leu Gly Gly Gly Ala Ile Leu
 485 490 495
 Ala Thr Gly Lys Val Glu Ile Thr Asn Asn Ser Gly Gly Ile Ser Phe
 500 505 510
 Thr Gly Asn Ala Arg Ala Pro Gln Ala Leu Pro Thr Gln Glu Glu Phe
 515 520 525
 Pro Leu Phe Ser Lys Lys Glu Gly Arg Pro Leu Ser Ser Gly Tyr Ser
 530 535 540
 Gly Gly Gly Ala Ile Leu Gly Arg Glu Val Ala Ile Leu His Asn Ala
 545 550 555 560
 Ala Val Val Phe Glu Gln Asn Arg Leu Gln Cys Ser Glu Glu Glu Ala
 565 570 575
 Thr Leu Leu Gly Cys Cys Gly Gly Ala Val His Gly Met Asp Ser
 580 585 590
 Thr Ser Ile Val Gly Asn Ser Ser Val Arg Phe Gly Asn Asn Tyr Ala
 595 600 605
 Met Gly Gln Gly Val Ser Gly Gly Ala Leu Leu Ser Lys Thr Val Gln

```

        610                615                620
Leu Ala Gly Asn Gly Ser Val Asp Phe Ser Arg Asn Ile Ala Ser Leu
625                630                635                640
Gly Gly Gly Ala Leu Gln Ala Ser Glu Gly Asn Cys Glu Leu Val Asp
        645                650                655
Asn Gly Tyr Val Leu Phe Arg Asp Asn Arg Gly Arg Val Tyr Gly Gly
        660                665                670
Ala Ile Ser Cys Leu Arg Gly Asp Val Val Ile Ser Gly Asn Lys Gly
        675                680                685
Arg Val Glu Phe Lys Asp Asn Ile Ala Thr Arg Leu Tyr Val Glu Glu
        690                695                700
Thr Val Glu Lys Val Glu Glu Val Glu Pro Ala Pro Glu Gln Lys Asp
705                710                715                720
Asn Asn Glu Leu Ser Phe Leu Gly Ser Val Glu Gln Ser Phe Ile Thr
        725                730                735
Ala Ala Asn Gln Ala Leu Phe Ala Ser Glu Asp Gly Asp Leu Ser Pro
        740                745                750
Glu Ser Ser Ile Ser Ser Glu Glu Leu Ala Lys Arg Arg Glu Cys Ala
755                760                765
Gly Gly Ala Asp Ser Ser Arg Ser Gly Cys
770                775

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<210> 194
 <211> 948
 <212> PRT
 <213> Chlamydia

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<400> 194
Met Ala Ser Met His His His His His Val Lys Ile Glu Asn Phe
1                5                10                15
Ser Gly Gln Gly Ile Phe Ser Gly Asn Lys Ala Ile Asp Asn Thr Thr
20                25                30
Glu Gly Ser Ser Ser Lys Ser Asn Val Leu Gly Gly Ala Val Tyr Ala
35                40                45
Lys Thr Leu Phe Asn Leu Asp Ser Gly Ser Ser Arg Arg Thr Val Thr
50                55                60
Phe Ser Gly Asn Thr Val Ser Ser Gln Ser Thr Thr Gly Gln Val Ala
65                70                75                80
Gly Gly Ala Ile Tyr Ser Pro Thr Val Thr Ile Ala Thr Pro Val Val
85                90                95
Phe Ser Lys Asn Ser Ala Thr Asn Asn Ala Asn Asn Ala Thr Asp Thr
100                105                110
Gln Arg Lys Asp Thr Phe Gly Gly Ala Ile Gly Ala Thr Ser Ala Val
115                120                125
Ser Leu Ser Gly Gly Ala His Phe Leu Glu Asn Val Ala Asp Leu Gly
130                135                140
Ser Ala Ile Gly Leu Val Pro Asp Thr Gln Asn Thr Glu Thr Val Lys
145                150                155                160
Leu Glu Ser Gly Ser Tyr Tyr Phe Glu Lys Asn Lys Ala Leu Lys Arg
165                170                175
Ala Thr Ile Tyr Ala Pro Val Val Ser Ile Lys Ala Tyr Thr Ala Thr
180                185                190
Phe Asn Gln Asn Arg Ser Leu Glu Glu Gly Ser Ala Ile Tyr Phe Thr
195                200                205
Lys Glu Ala Ser Ile Glu Ser Leu Gly Ser Val Leu Phe Thr Gly Asn
210                215                220
Leu Val Thr Pro Thr Leu Ser Thr Thr Thr Glu Gly Thr Pro Ala Thr
225                230                235                240

```

Thr Ser Gly Asp Val Thr Lys Tyr Gly Ala Ala Ile Phe Gly Gln Ile
 245 250 255
 Ala Ser Ser Asn Gly Ser Gln Thr Asp Asn Leu Pro Leu Lys Leu Ile
 260 265 270
 Ala Ser Gly Gly Asn Ile Cys Phe Arg Asn Asn Glu Tyr Arg Pro Thr
 275 280 285
 Ser Ser Asp Thr Gly Thr Ser Thr Phe Cys Ser Ile Ala Gly Asp Val
 290 295 300
 Lys Leu Thr Met Gln Ala Ala Lys Gly Lys Thr Ile Ser Phe Phe Asp
 305 310 315 320
 Ala Ile Arg Thr Ser Thr Lys Lys Thr Gly Thr Gln Ala Thr Ala Tyr
 325 330 335
 Asp Thr Leu Asp Ile Asn Lys Ser Glu Asp Ser Glu Thr Val Asn Ser
 340 345 350
 Ala Phe Thr Gly Thr Ile Leu Phe Ser Ser Glu Leu His Glu Asn Lys
 355 360 365
 Ser Tyr Ile Pro Gln Asn Val Val Leu His Ser Gly Ser Leu Val Leu
 370 375 380
 Lys Pro Asn Thr Glu Leu His Val Ile Ser Phe Glu Gln Lys Glu Gly
 385 390 395 400
 Ser Ser Leu Val Met Thr Pro Gly Ser Val Leu Ser Asn Gln Thr Val
 405 410 415
 Ala Asp Gly Ala Leu Val Ile Asn Asn Met Thr Ile Asp Leu Ser Ser
 420 425 430
 Val Glu Lys Asn Gly Ile Ala Glu Gly Asn Ile Phe Thr Pro Pro Glu
 435 440 445
 Leu Arg Ile Ile Asp Thr Thr Thr Ser Gly Ser Gly Gly Thr Pro Ser
 450 455 460
 Thr Asp Ser Glu Ser Asn Gln Asn Ser Asp Asp Thr Lys Glu Gln Asn
 465 470 475 480
 Asn Asn Asp Ala Ser Asn Gln Gly Glu Ser Ala Asn Gly Ser Ser Ser
 485 490 495
 Pro Ala Val Ala Ala Ala His Thr Ser Arg Thr Arg Asn Phe Ala Ala
 500 505 510
 Ala Ala Thr Ala Thr Pro Thr Thr Thr Pro Thr Ala Thr Thr Thr
 515 520 525
 Ser Asn Gln Val Ile Leu Gly Gly Glu Ile Lys Leu Ile Asp Pro Asn
 530 535 540
 Gly Thr Phe Phe Gln Asn Pro Ala Leu Arg Ser Asp Gln Gln Ile Ser
 545 550 555 560
 Leu Leu Val Leu Pro Thr Asp Ser Ser Lys Met Gln Ala Gln Lys Ile
 565 570 575
 Val Leu Thr Gly Asp Ile Ala Pro Gln Lys Gly Tyr Thr Gly Thr Leu
 580 585 590
 Thr Leu Asp Pro Asp Gln Leu Gln Asn Gly Thr Ile Ser Ala Leu Trp
 595 600 605
 Lys Phe Asp Ser Tyr Arg Gln Trp Ala Tyr Val Pro Arg Asp Asn His
 610 615 620
 Phe Tyr Ala Asn Ser Ile Leu Gly Ser Gln Met Ser Met Val Thr Val
 625 630 635 640
 Lys Gln Gly Leu Leu Asn Asp Lys Met Asn Leu Ala Arg Phe Asp Glu
 645 650 655
 Val Ser Tyr Asn Asn Leu Trp Ile Ser Gly Leu Gly Thr Met Leu Ser
 660 665 670
 Gln Val Gly Thr Pro Thr Ser Glu Glu Phe Thr Tyr Tyr Ser Arg Gly
 675 680 685
 Ala Ser Val Ala Leu Asp Ala Lys Pro Ala His Asp Val Ile Val Gly
 690 695 700

Ala Ala Phe Ser Lys Met Ile Gly Lys Thr Lys Ser Leu Lys Arg Glu
 705 710 715 720
 Asn Asn Tyr Thr His Lys Gly Ser Glu Tyr Ser Tyr Gln Ala Ser Val
 725 730 735
 Tyr Gly Gly Lys Pro Phe His Phe Val Ile Asn Lys Lys Thr Glu Lys
 740 745 750
 Ser Leu Pro Leu Leu Leu Gln Gly Val Ile Ser Tyr Gly Tyr Ile Lys
 755 760 765
 His Asp Thr Val Thr His Tyr Pro Thr Ile Arg Glu Arg Asn Gln Gly
 770 775 780
 Glu Trp Glu Asp Leu Gly Trp Leu Thr Ala Leu Arg Val Ser Ser Val
 785 790 795 800
 Leu Arg Thr Pro Ala Gln Gly Asp Thr Lys Arg Ile Thr Val Tyr Gly
 805 810 815
 Glu Leu Glu Tyr Ser Ser Ile Arg Gln Lys Gln Phe Thr Glu Thr Glu
 820 825 830
 Tyr Asp Pro Arg Tyr Phe Asp Asn Cys Thr Tyr Arg Asn Leu Ala Ile
 835 840 845
 Pro Met Gly Leu Ala Phe Glu Gly Glu Leu Ser Gly Asn Asp Ile Leu
 850 855 860
 Met Tyr Asn Arg Phe Ser Val Ala Tyr Met Pro Ser Ile Tyr Arg Asn
 865 870 875 880
 Ser Pro Thr Cys Lys Tyr Gln Val Leu Ser Ser Gly Glu Gly Gly Glu
 885 890 895
 Ile Ile Cys Gly Val Pro Thr Arg Asn Ser Ala Arg Gly Glu Tyr Ser
 900 905 910
 Thr Gln Leu Tyr Pro Gly Pro Leu Trp Thr Leu Tyr Gly Ser Tyr Thr
 915 920 925
 Ile Glu Ala Asp Ala His Thr Leu Ala His Met Met Asn Cys Gly Ala
 930 935 940
 Arg Met Thr Phe
 945

<210> 195

<211> 821

<212> PRT

<213> Chlamydia

<400> 195

Met His His His His His His Glu Ala Ser Ser Ile Gln Asp Gln Ile
 1 5 10 15
 Lys Asn Thr Asp Cys Asn Val Ser Lys Val Gly Tyr Ser Thr Ser Gln
 20 25 30
 Ala Phe Thr Asp Met Met Leu Ala Asp Asn Thr Glu Tyr Arg Ala Ala
 35 40 45
 Asp Ser Val Ser Phe Tyr Asp Phe Ser Thr Ser Ser Gly Leu Pro Arg
 50 55 60
 Lys His Leu Ser Ser Ser Ser Glu Ala Ser Pro Thr Thr Glu Gly Val
 65 70 75 80
 Ser Ser Ser Ser Ser Gly Glu Asn Thr Glu Asn Ser Gln Asp Ser Ala
 85 90 95
 Pro Ser Ser Gly Glu Thr Asp Lys Lys Thr Glu Glu Glu Leu Asp Asn
 100 105 110
 Gly Gly Ile Ile Tyr Ala Arg Glu Lys Leu Thr Ile Ser Glu Ser Gln
 115 120 125
 Asp Ser Leu Ser Asn Pro Ser Ile Glu Leu His Asp Asn Ser Phe Phe
 130 135 140
 Phe Gly Glu Gly Glu Val Ile Phe Asp His Arg Val Ala Leu Lys Asn

145 150 155 160
 Gly Gly Ala Ile Tyr Gly Glu Lys Glu Val Phe Glu Asn Ile Lys
 165 170 175
 Ser Leu Leu Val Glu Val Asn Ile Ser Val Glu Lys Gly Gly Ser Val
 180 185 190
 Tyr Ala Lys Glu Arg Val Ser Leu Glu Asn Val Thr Glu Ala Thr Phe
 195 200 205
 Ser Ser Asn Gly Gly Glu Gln Gly Gly Gly Ile Tyr Ser Glu Gln
 210 215 220
 Asp Met Leu Ile Ser Asp Cys Asn Asn Val His Phe Gln Gly Asn Ala
 225 230 235 240
 Ala Gly Ala Thr Ala Val Lys Gln Cys Leu Asp Glu Glu Met Ile Val
 245 250 255
 Leu Leu Thr Glu Cys Val Asp Ser Leu Ser Glu Asp Thr Leu Asp Ser
 260 265 270
 Thr Pro Glu Thr Glu Gln Thr Lys Ser Asn Gly Asn Gln Asp Gly Ser
 275 280 285
 Ser Glu Thr Lys Asp Thr Gln Val Ser Glu Ser Pro Glu Ser Thr Pro
 290 295 300
 Ser Pro Asp Asp Val Leu Gly Lys Gly Gly Ile Tyr Thr Glu Lys
 305 310 315 320
 Ser Leu Thr Ile Thr Gly Ile Thr Gly Thr Ile Asp Phe Val Ser Asn
 325 330 335
 Ile Ala Thr Asp Ser Gly Ala Gly Val Phe Thr Lys Glu Asn Leu Ser
 340 345 350
 Cys Thr Asn Thr Asn Ser Leu Gln Phe Leu Lys Asn Ser Ala Gly Gln
 355 360 365
 His Gly Gly Gly Ala Tyr Val Thr Gln Thr Met Ser Val Thr Asn Thr
 370 375 380
 Thr Ser Glu Ser Ile Thr Thr Pro Pro Leu Val Gly Glu Val Ile Phe
 385 390 395 400
 Ser Glu Asn Thr Ala Lys Gly His Gly Gly Gly Ile Cys Thr Asn Lys
 405 410 415
 Leu Ser Leu Ser Asn Leu Lys Thr Val Thr Leu Thr Lys Asn Ser Ala
 420 425 430
 Lys Glu Ser Gly Gly Ala Ile Phe Thr Asp Leu Ala Ser Ile Pro Thr
 435 440 445
 Thr Asp Thr Pro Glu Ser Ser Thr Pro Ser Ser Ser Pro Ala Ser
 450 455 460
 Thr Pro Glu Val Val Ala Ser Ala Lys Ile Asn Arg Phe Phe Ala Ser
 465 470 475 480
 Thr Ala Glu Pro Ala Ala Pro Ser Leu Thr Glu Ala Glu Ser Asp Gln
 485 490 495
 Thr Asp Gln Thr Glu Thr Ser Asp Thr Asn Ser Asp Ile Asp Val Ser
 500 505 510
 Ile Glu Asn Ile Leu Asn Val Ala Ile Asn Gln Asn Thr Ser Ala Lys
 515 520 525
 Lys Gly Gly Ala Ile Tyr Gly Lys Lys Ala Lys Leu Ser Arg Ile Asn
 530 535 540
 Asn Leu Glu Leu Ser Gly Asn Ser Ser Gln Asp Val Gly Gly Gly Leu
 545 550 555 560
 Cys Leu Thr Glu Ser Val Glu Phe Asp Ala Ile Gly Ser Leu Leu Ser
 565 570 575
 His Tyr Asn Ser Ala Ala Lys Glu Gly Gly Val Ile His Ser Lys Thr
 580 585 590
 Val Thr Leu Ser Asn Leu Lys Ser Thr Phe Thr Phe Ala Asp Asn Thr
 595 600 605
 Val Lys Ala Ile Val Glu Ser Thr Pro Glu Ala Pro Glu Glu Ile Pro

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        610                615                620
Pro Val Glu Gly Glu Glu Ser Thr Ala Thr Glu Asn Pro Asn Ser Asn
625                630                635                640
Thr Glu Gly Ser Ser Ala Asn Thr Asn Leu Glu Gly Ser Gln Gly Asp
        645                650                655
Thr Ala Asp Thr Gly Thr Gly Val Val Asn Asn Glu Ser Gln Asp Thr
        660                665                670
Ser Asp Thr Gly Asn Ala Glu Ser Gly Glu Gln Leu Gln Asp Ser Thr
        675                680                685
Gln Ser Asn Glu Glu Asn Thr Leu Pro Asn Ser Ser Ile Asp Gln Ser
        690                695                700
Asn Glu Asn Thr Asp Glu Ser Ser Asp Ser His Thr Glu Glu Ile Thr
705                710                715                720
Asp Glu Ser Val Ser Ser Ser Ser Lys Ser Gly Ser Ser Thr Pro Gln
        725                730                735
Asp Gly Gly Ala Ala Ser Ser Gly Ala Pro Ser Gly Asp Gln Ser Ile
        740                745                750
Ser Ala Asn Ala Cys Leu Ala Lys Ser Tyr Ala Ala Ser Thr Asp Ser
        755                760                765
Ser Pro Val Ser Asn Ser Ser Gly Ser Asp Val Thr Ala Ser Ser Asp
        770                775                780
Asn Pro Asp Ser Ser Ser Ser Gly Asp Ser Ala Gly Asp Ser Glu Gly
785                790                795                800
Pro Thr Glu Pro Glu Ala Gly Ser Thr Thr Glu Thr Pro Thr Leu Ile
        805                810                815
Gly Gly Gly Ala Ile
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<210> 196

<211> 525

<212> PRT

<213> Chlamydia

<400> 196

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Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
        35          40          45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
        50          55          60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
        65          70          75          80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
        85          90          95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
        100         105         110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
        115         120         125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Pro Leu Val Pro Arg Gly Ser
        130         135         140
Pro Leu Pro Val Gly Asn Pro Ala Glu Pro Ser Leu Leu Ile Asp Gly
        145         150         155         160
Thr Met Trp Glu Gly Ala Ser Gly Asp Pro Cys Asp Pro Cys Ala Thr
        165         170         175
Trp Cys Asp Ala Ile Ser Ile Arg Ala Gly Tyr Tyr Gly Asp Tyr Val
        180         185         190

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Phe Asp Arg Val Leu Lys Val Asp Val Asn Lys Thr Phe Ser Gly Met
 195 200 205
 Ala Ala Thr Pro Thr Gln Ala Ile Gly Asn Ala Ser Asn Thr Asn Gln
 210 215 220
 Pro Glu Ala Asn Gly Arg Pro Asn Ile Ala Tyr Gly Arg His Met Gln
 225 230 235 240
 Asp Ala Glu Trp Phe Ser Asn Ala Ala Phe Leu Ala Leu Asn Ile Trp
 245 250 255
 Asp Arg Phe Asp Ile Phe Cys Thr Leu Gly Ala Ser Asn Gly Tyr Phe
 260 265 270
 Lys Ala Ser Ser Ala Ala Phe Asn Leu Val Gly Leu Ile Gly Phe Ser
 275 280 285
 Ala Ala Ser Ser Ile Ser Thr Asp Leu Pro Met Gln Leu Pro Asn Val
 290 295 300
 Gly Ile Thr Gln Gly Val Val Glu Phe Tyr Thr Asp Thr Ser Phe Ser
 305 310 315 320
 Trp Ser Val Gly Ala Arg Gly Ala Leu Trp Glu Cys Gly Cys Ala Thr
 325 330 335
 Leu Gly Ala Glu Phe Gln Tyr Ala Gln Ser Asn Pro Lys Ile Glu Met
 340 345 350
 Leu Asn Val Thr Ser Ser Pro Ala Gln Phe Val Ile His Lys Pro Arg
 355 360 365
 Gly Tyr Lys Gly Ala Ser Ser Asn Phe Pro Leu Pro Ile Thr Ala Gly
 370 375 380
 Thr Thr Glu Ala Thr Asp Thr Lys Ser Ala Thr Ile Lys Tyr His Glu
 385 390 395 400
 Trp Gln Val Gly Leu Ala Leu Ser Tyr Arg Leu Asn Met Leu Val Pro
 405 410 415
 Tyr Ile Gly Val Asn Trp Ser Arg Ala Thr Phe Asp Ala Asp Thr Ile
 420 425 430
 Arg Ile Ala Gln Pro Lys Leu Lys Ser Glu Ile Leu Asn Ile Thr Thr
 435 440 445
 Trp Asn Pro Ser Leu Ile Gly Ser Thr Thr Ala Leu Pro Asn Asn Ser
 450 455 460
 Gly Lys Asp Val Leu Ser Asp Val Leu Gln Ile Ala Ser Ile Gln Ile
 465 470 475 480
 Asn Lys Met Lys Ser Arg Lys Ala Cys Gly Val Ala Val Gly Ala Thr
 485 490 495
 Leu Ile Asp Ala Asp Lys Trp Ser Ile Thr Gly Glu Ala Arg Leu Ile
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 Asn Glu Arg Ala Ala His Met Asn Ala Gln Phe Arg Phe
 515 520 525

<210> 197

<211> 43

<212> DNA

<213> Chlamydia

<400> 197

gataggcgcg cogcaatcat gaaatttatg tcagctactg ctg

43

<210> 198

<211> 34

<212> DNA

<213> Chlamydia

<400> 198

cagaacgcgt ttgaatgtc atacgagcac cgca

34

<210> 199
 <211> 6
 <212> DNA
 <213> Chlamydia

 <400> 199
 gcaatc 6

 <210> 200
 <211> 34
 <212> DNA
 <213> Chlamydia

 <400> 200
 tgcaatcatg agttcgcaga aagatataaa aagc 34

 <210> 201
 <211> 38
 <212> DNA
 <213> Chlamydia

 <400> 201
 cagagctagc ttaaaagatc aatcgcaatc cagtattc 38

 <210> 202
 <211> 5
 <212> DNA
 <213> Chlamydia

 <400> 202
 caatc 5

 <210> 203
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 <212> DNA
 <213> Chlamydia

 <400> 203
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 <210> 204
 <211> 31
 <212> DNA
 <213> Chlamydia

 <400> 204
 cagaacgcgt ctagaatcgc agagcaattt c 31

 <210> 205
 <211> 30
 <212> DNA
 <213> Chlamydia

 <400> 205
 gtgcaatcat gattcctcaa ggaatttacg 30

 <210> 206

<211> 31
 <212> DNA
 <213> Chlamydia

<400> 206
 cagaacgcgt ttagaaccgg actttacttc c 31

<210> 207
 <211> 50
 <212> DNA
 <213> Chlamydia

<400> 207
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<210> 208
 <211> 40
 <212> DNA
 <213> Chlamydia

<400> 208
 cagaggtacc tcagatagca ctctctccta ttaaagtagg 40

<210> 209
 <211> 55
 <212> DNA
 <213> Chlamydia

<400> 209
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<210> 210
 <211> 35
 <212> DNA
 <213> Chlamydia

<400> 210
 cagaggtacc ttagaatgtc atacgagcac cgcag 35

<210> 211
 <211> 36
 <212> DNA
 <213> Chlamydia

<400> 211
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<210> 212
 <211> 35
 <212> DNA
 <213> Chlamydia

<400> 212
 cagaggtacc tcagctctc cagcacactc tcttc 35

<210> 213
 <211> 51
 <212> DNA

<213> Chlamydia

<400> 213
cagagctagc catcaccatc accatcacgg tgctatttct tgcttacgtg g 51

<210> 214
<211> 38
<212> DNA
<213> Chlamydia

<400> 214
cagaggtact taaaagatca atcgcaatcc agtattcg 38

<210> 215
<211> 48
<212> DNA
<213> Chlamydia

<400> 215
cagaggatcc acatcaccat caccatcacg gactagctag agaggttc 48

<210> 216
<211> 31
<212> DNA
<213> Chlamydia

<400> 216
cagagaattc ctagaatcgc agagcaattt c 31

<210> 217
<211> 7
<212> DNA
<213> Chlamydia

<400> 217
tgcaatc 7

<210> 218
<211> 22
<212> PRT
<213> Chlamydia

<400> 218
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1 5 10 15
Val Pro Ser Ser Asp Pro
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<210> 219
<211> 51
<212> DNA
<213> Chlamydia

<400> 219
cagaggtagc gcataccat caccatcaca tgattcctca aggaatttac g 51

<210> 220
<211> 33

<212> DNA
<213> Chlamydia

<400> 220
cagagcggcc gcttagaacc ggactttact tcc 33

<210> 221
<211> 24
<212> PRT
<213> Chlamydia

<400> 221
Met Ala Ser Met Thr Gly Gly Gln Gln Asn Gly Arg Asp Ser Ser Leu
1 5 10 15
Val Pro His His His His His His
20

<210> 222
<211> 46
<212> DNA
<213> Chlamydia

<400> 222
cagagctagc catcaccatc accatcacct ctttgccag gatccc 46

<210> 223
<211> 30
<212> DNA
<213> Chlamydia

<400> 223
cagaactagt ctagaacctg taagtgggcc 30

<210> 224
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 224
Met Ser Gln Lys Asn Lys Asn Ser Ala Phe Met His Pro Val Asn Ile
1 5 10 15
Ser Thr Asp Leu
20

<210> 225
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 225
Lys Asn Ser Ala Phe Met His Pro Val Asn Ile Ser Thr Asp Leu Ala
1 5 10 15

Val Ile Val Gly
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<210> 226
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 226
His Pro Val Asn Ile Ser Thr Asp Leu Ala Val Ile Val Gly Lys Gly
1 5 10 15
Pro Met Pro Arg
20

<210> 227
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 227
Ser Thr Asp Leu Ala Val Ile Val Gly Lys Gly Pro Met Pro Arg Thr
1 5 10 15
Glu Ile Val Lys
20

<210> 228
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 228
Val Ile Val Gly Lys Gly Pro Met Pro Arg Thr Glu Ile Val Lys Lys
1 5 10 15
Val Trp Glu Tyr
20

<210> 229
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 229
Gly Pro Met Pro Arg Thr Glu Ile Val Lys Lys Val Trp Glu Tyr Ile
1 5 10 15
Lys Lys His Asn
20

<210> 230
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 230
 Ile Lys Lys His Asn Cys Gln Asp Gln Lys Asn Lys Arg Asn Ile Leu
 1 5 10 15
 Pro Asp Ala Asn
 20

<210> 231
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 231
 Asn Cys Gln Asp Gln Lys Asn Lys Arg Asn Ile Leu Pro Asp Ala Asn
 1 5 10 15
 Leu Ala Lys Val
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<210> 232
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 232
 Lys Asn Lys Arg Asn Ile Leu Pro Asp Ala Asn Leu Ala Lys Val Phe
 1 5 10 15
 Gly Ser Ser Asp
 20

<210> 233
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 233
 Ile Leu Pro Asp Ala Asn Leu Ala Lys Val Phe Gly Ser Ser Asp Pro
 1 5 10 15
 Ile Asp Met Phe
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<210> 234

<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 234
Asn Leu Ala Lys Val Phe Gly Ser Ser Asp Pro Ile Asp Met Phe Gln
1 5 10 15
Met Thr Lys Ala
20

<210> 235
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 235
Phe Gly Ser Ser Asp Pro Ile Asp Met Phe Gln Met Thr Lys Ala Leu
1 5 10 15
Ser Lys His Ile Val Lys
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<210> 236
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 236
Val Glu Ile Thr Gln Ala Val Pro Lys Tyr Ala Thr Val Gly Ser Pro
1 5 10 15
Tyr Pro Val Glu
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<210> 237
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 237
Ala Val Pro Lys Tyr Ala Thr Val Gly Ser Pro Tyr Pro Val Glu Ile
1 5 10 15
Thr Ala Thr Gly
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<210> 238
<211> 20
<212> PRT

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<220>

<223> Made in a lab

<400> 238

Ala Thr Val Gly Ser Pro Tyr Pro Val Glu Ile Thr Ala Thr Gly Lys
1 5 10 15
Arg Asp Cys Val
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<210> 239

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 239

Pro Tyr Pro Val Glu Ile Thr Ala Thr Gly Lys Arg Asp Cys Val Asp
1 5 10 15
Val Ile Ile Thr
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<210> 240

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 240

Ile Thr Ala Thr Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln
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Gln Leu Pro Cys Glu
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<210> 241

<211> 20

<212> PRT

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<220>

<223> Made in a lab

<400> 241

Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln Gln Leu Pro Cys Glu
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Ala Glu Phe Val
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<210> 242

<211> 20

<212> PRT

<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 242
Asp Val Ile Ile Thr Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Arg
1 5 10 15
Ser Asp Pro Ala
20

<210> 243
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 243
Thr Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Arg Ser Asp Pro Ala
1 5 10 15
Thr Thr Pro Thr
20

<210> 244
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 244
Cys Glu Ala Glu Phe Val Arg Ser Asp Pro Ala Thr Thr Pro Thr Ala
1 5 10 15
Asp Gly Lys Leu
20

<210> 245
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 245
Val Arg Ser Asp Pro Ala Thr Thr Pro Thr Ala Asp Gly Lys Leu Val
1 5 10 15
Trp Lys Ile Asp
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<210> 246
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 246
Ala Thr Thr Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg
1 5 10 15
Leu Gly Gln Gly
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<210> 247
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 247
Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln Gly Glu
1 5 10 15
Lys Ser Lys Ile
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<210> 248
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 248
Val Trp Lys Ile Asp Arg Leu Gly Gln Gly Glu Lys Ser Lys Ile Thr
1 5 10 15
Val Trp Val Lys
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<210> 249
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 249
Arg Leu Gly Gln Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro
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Leu Lys Glu Gly
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<210> 250
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 250

Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly
1 5 10 15
Cys Cys Phe Thr
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<210> 251
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 251
Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly
1 5 10 15

<210> 252
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 252
Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly
1 5 10

<210> 253
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 253
Gly Asp Lys Cys Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly
1 5 10 15

<210> 254
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 254
Thr Glu Tyr Pro Leu Leu Ala Asp Pro Ser Phe Lys Ile Ser Glu Ala
1 5 10 15
Phe Gly Val Leu
20

<210> 255
<211> 20
<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 255

Leu Ala Asp Pro Ser Phe Lys Ile Ser Glu Ala Phe Gly Val Leu Asn
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Pro Glu Gly Ser
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<210> 256

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 256

Phe Lys Ile Ser Glu Ala Phe Gly Val Leu Asn Pro Glu Gly Ser Leu
1 5 10 15
Ala Leu Arg Ala
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<210> 257

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 257

Ala Phe Gly Val Leu Asn Pro Glu Gly Ser Leu Ala Leu Arg Ala Thr
1 5 10 15
Phe Leu Ile Asp
20

<210> 258

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 258

Asn Pro Glu Gly Ser Leu Ala Leu Arg Ala Thr Phe Leu Ile Asp Lys
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His Gly Val Ile
20

<210> 259

<211> 20

<212> PRT

<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 259
Leu Ala Leu Arg Ala Thr Phe Leu Ile Asp Lys His Gly Val Ile Arg
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His Ala Val Ile
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<210> 260
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 260
Thr Phe Leu Ile Asp Lys His Gly Val Ile Arg His Ala Val Ile Asn
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Asp Leu Pro Leu
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<210> 261
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 261
Lys His Gly Val Ile Arg His Ala Val Ile Asn Asp Leu Pro Leu Gly
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Arg Ser Ile Asp
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<210> 262
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 262
Arg His Ala Val Ile Asn Asp Leu Pro Leu Gly Arg Ser Ile Asp Glu
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Glu Leu Arg Ile
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<210> 263
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<212> DNA
<213> Chlamydia

<220>
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gcgggctctt	ccgcacacat	tacagcttcc	caagtgtcca	aaggattagg	ggatgcgaga	240
actgtgtctg	ctttaggga	tgcccttaac	ggagcgttgc	caggaacagt	tcaaatgtgc	300
caaagcttct	tctctcacat	gaaagctgct	agtcagaaaa	cgcaagaagg	ggatgagggg	360
ctcacagcag	atctttgtgt	gtctcataag	cgcagagcgg	ctgcggctgt	ctgtagcatc	420
atcggaggaa	ttacctacct	cgcgacattc	ggagctatcc	gtccgattct	gtttgtcaac	480
aaaatgctgg	caaaaccgtt	tcctttctcc	caaatcaaa	caaatattgg	atcttctgtt	540
agctatatta	tgccggctaa	ccatgcagcg	tctgtgtgtg	gtgctggact	cgctatcagt	600
gcgnaaaag	cagattgcga	agcccgctgc	gctcgtattg	cgagagaaga	gtcgttactc	660
gaagtgcggg	gagaggaaaa	tgcttgcgag	aagaaagtgc	ctggagagaa	agccaagacg	720
ttcacgcgca	tcaagtatgc	actcctcact	atgctcgaga	agtttttggg	atgcggttgc	780
gacgttttca	aattggtgcc	gctgcctatt	acaatgggta	ctcgtgcgat	tgtggctgct	840
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<210> 264

<211> 298

<212> PRT

<213> Chlamydia

<220>

<221> VARIANT

<222> (1) ... (298)

<223> Xaa = Any Amino Acid

<400> 264

Met	Ala	Ser	Ile	Cys	Gly	Arg	Leu	Gly	Ser	Gly	Thr	Gly	Asn	Ala	Leu
1				5					10					15	
Lys	Ala	Phe	Phe	Thr	Gln	Pro	Asn	Asn	Lys	Met	Ala	Arg	Val	Val	Asn
			20					25					30		
Lys	Thr	Lys	Gly	Val	Asp	Lys	Thr	Ile	Lys	Val	Ala	Lys	Ser	Ala	Ala
		35					40					45			
Glu	Leu	Thr	Ala	Asn	Ile	Leu	Glu	Gln	Ala	Gly	Gly	Ala	Gly	Ser	Ser
	50					55					60				
Ala	His	Ile	Thr	Ala	Ser	Gln	Val	Ser	Lys	Gly	Leu	Gly	Asp	Ala	Arg
65					70				75					80	
Thr	Val	Val	Ala	Leu	Gly	Asn	Ala	Phe	Asn	Gly	Ala	Leu	Pro	Gly	Thr
				85					90					95	
Val	Gln	Ser	Ala	Gln	Ser	Phe	Phe	Ser	His	Met	Lys	Ala	Ala	Ser	Gln
			100					105					110		
Lys	Thr	Gln	Glu	Gly	Asp	Glu	Gly	Leu	Thr	Ala	Asp	Leu	Cys	Val	Ser
		115				120					125				
His	Lys	Arg	Arg	Ala	Ala	Ala	Ala	Val	Cys	Ser	Ile	Ile	Gly	Gly	Ile
	130					135					140				
Thr	Tyr	Leu	Ala	Thr	Phe	Gly	Ala	Ile	Arg	Pro	Ile	Leu	Phe	Val	Asn
145					150				155					160	
Lys	Met	Leu	Ala	Lys	Pro	Phe	Leu	Ser	Ser	Gln	Thr	Lys	Ala	Asn	Met
				165				170						175	
Gly	Ser	Ser	Val	Ser	Tyr	Ile	Met	Ala	Ala	Asn	His	Ala	Ala	Ser	Val
			180					185					190		
Val	Gly	Ala	Gly	Leu	Ala	Ile	Ser	Ala	Xaa	Arg	Ala	Asp	Cys	Gly	Ala
		195				200					205				
Arg	Cys	Ala	Arg	Ile	Ala	Arg	Glu	Glu	Ser	Leu	Leu	Glu	Val	Pro	Gly

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      210              215              220
Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr
225              230              235              240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
      245              250              255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
      260              265              270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
      275              280              285
Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
      290              295

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<210> 265

<211> 897

<212> DNA

<213> Chlamydia

<220>

<221> misc_feature

<222> (1)...(897)

<223> n = A,T,C or G

<400> 265

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acacagccca acaataaaat ggcaagggtg gtaataaaga cgaagggaat ggataagact      120
attaaggttg ccaagtctgc tgccgaattg accgcaaaat ttttggaaca agctggaggc      180
gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggaatgcgaga      240
actgtgtctg ctttagggaa tgccotttaac ggagcgttgc caggaaacagt tcaaatgtcg      300
caaaagcttc tctctcacat gaaagctgct agtcagaaaa cgcaagaagg ggaatgaggg      360
ctcacaggag atcttttgtg gtctcataag cgcagagcgg ctgcggtgtg ctgtagcatt      420
atcggaggaa ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac      480
aaaatgctgg caaaaccgtt tctttcttcc caaactaaag caaatatggg atcttctgtt      540
agctatatta tggcggctaa ccatgcagcg tctgtgtgtg gtgctggact cgctatcagt      600
gcgnaaagag cagattgcga agcccgtctg gctcgtattg cgagagaaga gtcttactc      660
gaagtgccgg gagagggaaa tgcttgcgag aagaaaagtc ctggagagaa agccaagacg      720
ttcaocgcga tcaagtatgc actcctcact atgctcgaga agtttttggg atgcgttgcc      780
gacgttttca aattggtgcc gctgcctatt acaatgggta ttctgtcgat tgtggtgtct      840
ggatgtacgt tcacttctgc aattattgga ttgtgcactt tctgcgcag agcataa      897

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<210> 266

<211> 298

<212> PRT

<213> Chlamydia

<220>

<221> VARIANT

<222> (1)...(298)

<223> Xaa = Any Amino Acid

<400> 266

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Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
  1              5              10              15
Lys Ala Phe Phe Thr Gln Pro Asn Asn Lys Met Ala Arg Val Val Asn
  20              25              30
Lys Thr Lys Gly Met Asp Lys Thr Ile Lys Val Ala Lys Ser Ala Ala
  35              40              45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
  50              55              60

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Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
 65 70 75 80
 Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
 85 90 95
 Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
 100 105 110
 Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
 115 120 125
 His Lys Arg Arg Ala Ala Ala Val Cys Ser Ile Ile Gly Gly Ile
 130 135 140
 Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
 145 150 155 160
 Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
 165 170 175
 Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
 180 185 190
 Val Gly Ala Gly Leu Ala Ile Ser Ala Xaa Arg Ala Asp Cys Glu Ala
 195 200 205
 Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Pro Gly
 210 215 220
 Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr
 225 230 235 240
 Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
 245 250 255
 Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
 260 265 270
 Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
 275 280 285
 Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
 290 295

<210> 267

<211> 680

<212> DNA

<213> Chlamydia

<400> 267

tctatatcca	tattgatagg	aaaaaacgtc	gcagaaagat	tttagctatg	acgttttatcc	60
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gttcctttacg	tcagagaag	gattttgtcg	cgtttagtgg	taaaagtttta	gctgataaac	180
tgatttgatg	ggattcttca	ttagtttaacg	ggaaagctgg	agagaagcta	agctactgcta	240
tgctaaaaacg	catcttagat	acggggagtc	aatctttgaa	gattgctggt	ggcgagatg	300
aaaatcacc	aattattaag	atgctcgcaa	aagatcctac	ggattctttac	gaagctgctc	360
ttaaagattt	ttatcgcaga	ttacgaccag	gagagcctgc	aactttagct	aatgctcgat	420
ccacaattat	gcgtttatc	ttcgatgcta	aacgttataa	tttaggcgcg	gttggacgtt	480
ataaattaaa	taaaaaatta	ggcttcccat	tagacgacga	aacattatct	caagtgaact	540
tgagaaaaga	agatgtttatc	ggcgcggtga	aatatttgat	tcgttttgca	atggcgatg	600
agaagacatc	tatcgatgat	attgaccatt	tggcaaacgc	acgagttcgc	tctgttggag	660
aactaatcca	gaatcactgt					680

<210> 268

<211> 359

<212> DNA

<213> Chlamydia

<400> 268

cttatgttct	ggagaatggt	gcaacaacat	attaatcgaa	ccagctcctc	ctagtaacat	60
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agctcctaac	aagagctaa	tttttctctc	ttccttgttt	ttctgaggcg	ctgtgggactc	180
taaataatagc	aagtgtctct	ggaacacctc	atcaacaatc	gcttgtccta	gattaggtat	240
agagactgtc	tctccatcaa	ttaaattggag	tttcaaaagta	atatcccttc	ccgtccctcc	300
atcacaagac	tctatgaaag	ctatctgatt	ccatcgagca	gaaatgtatg	gggaaatc	359

<210> 269

<211> 124

<212> DNA

<213> Chlamydia

<400> 269

gatcgaatca	attgagggag	ctcattaaca	agaatagctg	cagttctctt	gcgttctctt	60
ggataatacaa	gaaataggtt	atcggtacca	tgatagaaac	gaacacgaca	aatcgcgaaa	120
ggtt						124

<210> 270

<211> 219

<212> DNA

<213> Chlamydia

<400> 270

gatcctgttg	ggcctagtaa	taatacgttg	gatttcccat	aactcacttg	tttatcctgc	60
ataagagcac	ggatagcgtt	atagtgggtt	tagacggcaa	ccgaaatcgt	ttttttcgcg	120
cgctcttgct	caatgacata	agagtcgatg	tggcgtttga	tttcttttagg	ggttaacact	180
ctcagacttg	ttggagagct	tgtggaagat	gttgcgcatc			219

<210> 271

<211> 511

<212> DNA

<213> Chlamydia

<220>

<221> misc_feature

<222> (1) ... (511)

<223> n = A,T,C or G

<400> 271

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acaaagaggt	tttggcatag	atggctctct	cttgtagctt	caacgatgat	tgggagggat	120
tgttatcgat	agcttggctc	ccagagaaact	gacaagtccc	gctacattga	gagaattgtaa	180
ctctttctcc	atagatagct	cctcctacta	cacctgaata	agttgggtgt	gctggagatg	240
atggtgcggc	tgctgcggtc	gctttagtagg	aagcagcagc	tgacagcaggt	gctgaagctg	300
ttgttgcgac	tcctgtggat	gaggagtttg	ctttgttgtt	cgagaaaagag	aagcctgatt	360
tcagattaga	aataattaca	gttttagcat	gtaagcctcc	accctctctc	ccaacaaggt	420
tctctgttac	agataaggag	actagangca	tctagtttta	aagatttttt	acagcagata	480
cctccaccta	tctctgtagc	ggagttctca	g			511

<210> 272

<211> 598

<212> DNA

<213> Chlamydia

<400> 272

ctcttctctc	cctcaatcta	gttctggagc	aactacagtc	tcgactcag	gagactctag	60
ctctgggtca	aactcggata	cctcaaaaac	agttccagtc	acagctaaag	cggttgggct	120
ttatactgat	aagaatcttt	cgattactaa	catcacagga	attatcgaaa	ttgcaaataa	180
caaaacgaca	gatgttggag	gtggtgctta	cgtaaaagga	acccttactt	gtaaaaactc	240
tcaccgtcta	caatttttga	aaaactcttc	cgataaaaca	ggtggaggaa	tctacggaga	300

agacaacatc	acccatctcta	atttgacagg	gaagactcta	ttccaagaga	atactgccaa	360
aaaagagggc	ggtggactct	tcataaaagg	tacagataaa	gctcttcaaa	tgacaggact	420
ggatagtctc	tgtttaatta	ataacacatc	agaaaaacat	ggtgggggga	gcctttgtta	480
ccaaagaaat	ctctcagaat	tacacctctt	gatgtggaaa	caattccagg	aatcacgcct	540
gtacatggcg	aaacagcctat	tactggcaat	aaatctacag	gaggtaatgg	tgaggggc	598

<210> 273

<211> 126

<212> DNA

<213> Chlamydia

<400> 273

ggatccgaat	tcggcagcag	atgagcctta	tagtttaaca	aaagctttct	acattccttc	60
gatagctttt	tattagcgtt	ttttagcctc	ctaattgagat	ctctctgttc	gtaacaaata	120
cgagag						126

<210> 274

<211> 264

<212> DNA

<213> Chlamydia

<400> 274

ggatccgaat	tcggcagcag	ctctttttaa	ttttaattac	aaaaagacaa	atttaattcaa	60
tttttcaaaa	aagaatttaa	acatttaattg	ttgtaaaaaa	acaatattta	ttctaaaaata	120
ataacacatg	ttacggggga	atctctttca	tggtttattt	tagagctcat	caacctaggg	180
atagccttaa	aacattttct	ttgaaagttc	accattcggt	ctcgcataag	catctctcaa	240
ttgctaaagc	tatgtggatt	acgg				264

<210> 275

<211> 359

<212> DNA

<213> Chlamydia

<400> 275

ggatccgaat	tcggcagcag	ataaaacctg	aaccacaaca	aagatctaaa	acttcttgat	60
tttcagctgc	aaattctttt	agataaatat	caaccatttc	ttcagtttca	tatcttggaa	120
ttaaaacttg	ttctctttaa	tttaattctag	tatttaagta	ttcaacatag	ccatttatta	180
attgaattgg	ataattttgc	ottaataatt	cacattcttt	ttcagtaatt	ttaggttcta	240
aaccgtaccg	ctttttttct	aaaattaatg	tttcttcat	atcattttta	taagccactt	300
tccttttatt	tttgattttg	ttcttctggt	agtaatgctt	caataatagt	taataatttt	359

<210> 276

<211> 357

<212> DNA

<213> Chlamydia

<400> 276

aaaacaattg	atataatttt	ttttttcata	acttcacagc	tcctttctag	aaaagtcttt	60
atgggtagta	gtgactctaa	cgttttttat	tattaagagc	atccccgag	atccttttaa	120
tgatgaaac	ggaacatcc	tttcgcaga	aacttttagc	ctattaaaga	atcggtacgg	180
gttagataag	cttttatcca	cccagtatct	tatctatttg	aaatgtctgc	taacactaga	240
tttcggggaa	ttctttatct	acaaagatcg	aaatctcagc	attattgctg	cgctctttcc	300
atcttccgct	attcttggac	ttgaaagcct	gtgtttactc	gtgccgaatt	cggatccc	357

<210> 277

<211> 505

<212> DNA

<213> Chlamydia

<400> 277
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 ggtaaaaaatc ctaaggccat accaggatgc gacaggaaag agatatctcc attagggaatg 180
 cggagacacg ctgggtttgtg gccacaagaa tagtattcta gttctcgtgt tgcgtaatga 240
 taacaataaaa tgcatagtgt tacaacatc ccagattcag ctgtctgttg atagaagaga 300
 gcagctgttt gttgaacggc ttcttgaata gaggagagct cactcaaaaa ggatgttaac 360
 atgtttttca ggaataagga gtaggcgacg gcattgactc ctttcccgga agcatcagca 420
 acgattagaa agagttttagc ttggggacct tcgcctataa caaagatatc aaagaaatct 480
 cctcctaccg taactgcagc aatat 505

<210> 278
 <211> 407
 <212> DNA
 <213> Chlamydia

<400> 278
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 aagaaaaaca gaaggcattc tccataccaa gatttggtgc atcgacaata aaactccaat 120
 ctttggctct gctaactgga gcgggtgctgg tatgattaaa aactttgagg acctattcat 180
 ccttcgcccc attacagaga cacagcttca ggcccttatg gacgtctggt ctctctcaga 240
 aacaaatagc tcctatctgt cccagagagc cgtgcttacg gccctactc cttcaagtag 300
 acctactcaa caagatacag attctgatga cgaacaccc agtaccagcc agcaagctat 360
 ccgtatgaga aaataggatt agggaaaaca aacgacagca aaccaca 407

<210> 279
 <211> 351
 <212> DNA
 <213> Chlamydia

<400> 279
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 tggcgatagg ccgggtctag ccgcgatagt agaaatatcg gttggttttt gtccttgagg 120
 ggatcgata ctttttcaaa gtatggtccc cgtatcgatt atctggaggc tcttatgtct 180
 ttttttcaata ctagaaaata taagcttacc ctcagaggac tcttgtgttt agcaggctgt 240
 ttcttaataga acagctgttc ctctagtcga ggaaatcaac ccgctgatga gagcatctat 300
 gtcttgtcta tgaatcgcat gattttgtgat tctctgccc aattcggatc c 351

<210> 280
 <211> 522
 <212> DNA
 <213> Chlamydia

<400> 280
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 agaagatctt tcogaagtct ctggagaaga ttttcgagga ttgaaaaatt cggtcgatga 120
 tgattctctc tctgacgaaa ttctcgatgc gctcacaagt aaattttctt atccccaat 180
 aaaggatcta gctcttgatt atctaattca aatagctccc tctgatggga aacttaagt 240
 cgctctcatt caggcaaacg atcaactgat gagccagaat cctcaggcga ttgttgagg 300
 acgcaatgct ctgttagctt cagaaacctt tgcttccaga gcaaatatcat ctctctcctc 360
 gcttcgcttc ttatatttcc aagtaacctc atccccctc ttattcgcta atttacatca 420
 aatgcttgct tcttactcgc catcagagaa aaccgctgtt atggagtttc tagtgaatgg 480
 catggtagca gatttaaaat cggaggggcc tccattcct cc 522

<210> 281
 <211> 577
 <212> DNA

<213> Chlamydia

<400> 281

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ccagcttatt	ctagaaaaagt	tgggagatca	aattcttggg	ggaattgctg	atactattgt	120
tgatagtaca	gtccaaagata	tttttagacaa	aatcacaaca	gaccttcttc	taggtttgtt	180
gaaagctttt	aacaactttc	caatcactaa	taaaattcaa	tgcaacgggt	tattcactcc	240
caggaacatt	gaaactttat	taggaggaac	tgaaatagga	aaattcacag	tcacacccaa	300
aagctctggg	agcatgtttc	tagtctcagc	agatattatt	gcatacagaa	tgggaaggcg	360
ogttgttcta	gctttggatc	gagaagggtga	ttctaagccc	tacgcgatta	gttatggata	420
ctcactcagg	gttctcaatt	tatgtagtct	aagaaccaga	attattaata	caggattgac	480
tcgcacaacg	tattcattac	gtgtaggcgg	tttagaaaag	gggtgtggat	gggttaatgc	540
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<210> 282

<211> 607

<212> DNA

<213> Chlamydia

<400> 282

actmatcttc	ccggggctcg	agtgcggcgg	caagcttgctc	gacggagctc	gatacaaaaa	60
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gccattcaaa	taattgtccc	aagcccatct	gtacttaata	ggacaacagt	ggttgacatc	360
gacctgggtg	cagttcctac	gacgcttgct	atttagatta	acgcgtttct	gttttccatc	420
taaaaatatt	gcttgcataa	gaaccgttaa	ttttattgtt	aatttatatt	attataattc	480
gacatgcttc	acaccctctc	tccaaagAAC	agacaggtgc	tttcttcgct	ctttcaacaa	540
taattctctg	cgaagcagac	ttattcttca	tcacaagagg	ctgaattctc	cttttattaa	600
tattctac						607

<210> 283

<211> 1077

<212> DNA

<213> Chlamydia

<400> 283

ggatccgaat	tcggcagcag	aagttaacga	tgacgatttg	ttctcttggg	agagaaggag	60
caatcgaaac	taaatgtggc	agagcatgtg	aagactccaa	tgacgaataa	atccccctat	120
ttctagttaa	caggaaaaaa	gctcgttaac	ctctctctac	gggtggctaat	gtataaaaag	180
ctcgtctcga	ctcatgcat	tcggcatgat	ctggcccaac	tgaaagataa	tctaatacag	240
cggaaatgga	gtgagtttgt	aataacttgtc	catcgtctac	ttgaagaaga	tacgaataaa	300
atccgtggaa	tactccaggt	cgccctgttg	caaaacgtgc	tgcatgtttt	ctcgaagaaa	360
tgcccagctc	ctccccctac	actccaatta	attggacttt	tggtatccgg	ataaaatgat	420
ggaaaaatcc	aatagcgttg	gagccacctc	cgatacatgc	aatcagaata	tcaggatctc	480
ttctctgaac	tgcatggatt	tgctctttca	cttcagcgct	tataacagac	tgaaaaaatc	540
gaacgataat	gggataaggt	aaaggtccta	aggccgatcc	taagcaaatg	tcagtaaatg	600
agtggtgtgt	tgcccaactc	tgtagagctt	gattaaactgc	attcttgagt	ccacaagatc	660
cttttgtttc	agaaaagact	tcagcaccta	aaaagcgcac	tttctctaca	tttggtttct	720
gtcgttccac	atctttttgt	cccatgtata	ctacacaact	taactctaga	taagcacacg	780
ttctgtctgt	tgctactcca	tggtgtcccg	caactgtttc	agctacaaca	cgtgtttttc	840
caagatattt	agcaagcaaa	cactgaccaa	gagcattatt	cagtttatgt	gtcctgtgat	900
gcaaaagatc	ttcgcgttta	agaaatactc	tagggccatc	aatagctcga	gcaaaattct	960
taacttcagt	cagaggagtt	tgtctccccc	catagttttt	caaaatacaa	tctagttcag	1020
ataaaaaact	ttgctgagtt	ttgagaactc	ccattccgcg	tttagatttc	tgtatag	1077

<210> 284

<211> 407
 <212> DNA
 <213> Chlamydia

<400> 284
 ggatccgaat tcggcacgag aactactgag caaattgggt atccaaacttc ctctttacga 60
 aagaaaaaca gaaggcattc tccataccaa gatattgttg atcgacaata aaactccaat 120
 ctttggctct gctaaactgga cgggtgctgg tatgattaaa aactttgaag acctattcat 180
 ccttcgcccc attacagaga cacagcttca gccctttatg gacgtctggt ctctctctaga 240
 aacaaatagc tcttatctgt cccagagag cgtgcttacg gccctacttc ctccaagtag 300
 acctactcaa caagatacag attctgatga cgaacaaccg agtaccagcc agcaagctat 360
 ccgtatgaga aaataggatt agggaaacaa aacgacagca aaccaca 407

<210> 285
 <211> 802
 <212> DNA
 <213> Chlamydia

<400> 285
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 taattctaca ggcacaattg gaatcgtaa ttacgtcgc tgcctagaag agtctgctct 120
 ttgggaaaaa gaatctgctg aatttcgaaa gatgaaaaac caattctctc acagcatggg 180
 gaagatggag gaagaactgt ctctctatcta ttccaagctc caagacgacg attacatgga 240
 aggtctctcc gagacgcgag ctgcgcgaatt aagaaaaaaa ttccaagatc tatctgcaga 300
 atacaacaca gctcaagggc agtattacca aatattaaac caaagtaatc tcaagcgcatt 360
 gcaaaagatt atggaagaag tgaaaaaagc ttctgaaact gtgcgtattc aagaaggctt 420
 gtcaagctct cttaacgag atattgtctt atctatcgat agttcggcag ataaaaaccga 480
 tgcgtctatt aaagtctctg atgattcttt tcaaaataat taacatgcga agctagccga 540
 ggagtgcggt atgtctcaat ccactttatc tcttgaacaa ttagctgatt ttttgaagat 600
 cgagtcttca ggaataggag ctactctctt ttcggaggtt gaagagatcg aggaagcaaa 660
 aacggcacac atcacattct tagataatga aaaatatgct aaacatttaa aatcatcgga 720
 agctggcgct atcatcatat ctggaacaca gtttcaaaaa tatcgagact tgaataaaaa 780
 cttctctatc acttctgagt ct 802

<210> 286
 <211> 588
 <212> DNA
 <213> Chlamydia

<400> 286
 ggatccgaat tcggcacgag gcaatattta ctcccaacat tacggttcca aataagcgat 60
 aaggctctct aataagggaag ttaattgtaag aggccttttt atgtcttttc gtaaggtagt 120
 attgcaaccg cagcgcattg aatgatacgc aagccatttc catcatggaa aagaaccttt 180
 ggacaaaaat acaaggaggg ttcaactccta accagaaaaa gggagagtta gtttccatgg 240
 gttttcctta tatacacccg ttcaacacaa ttaggagccg cgtctagtat ttggaataga 300
 aattgtcccc aagcgaattt tgttctctgt tcagggaatt ctctcaattg tctgtctcag 360
 catcgcctca tggtaacgca attagctgta gtaggaaagt caactccaaa caggtcatag 420
 aaatcagaaa gctcataggt gctcgcgca atacaacat tcttctctga gtgacggaat 480
 tgtttaaaag atggggcgat atgagctacc tcatcagaga ctattttaaa tagatcattt 540
 tgggtaatca atccttctat agaccatcat tcatcaatga taatctcgy 588

<210> 287
 <211> 489
 <212> DNA
 <213> Chlamydia

<220>
 <221> misc_feature

<222> (1) ... (489)

<223> n = A, T, C or G

```

<400> 287
agtgcctatt gttttgcagc ctttgtctga tgatagcgat accgtacgtg agattgctgt      60
acaagtagct gttatgtatg gttctagtgt ctactgcgc gccgtgggcg atttagcgaa      120
aaatgattct tctattcaag tacgcatcac tgcctatcgt gctgcagcgc gttggagagt      180
acaagatctt gtgcctcatt tacgagttgt agtccaaaat acacaattag atggaaacgga      240
aagaagagaa gcttggagat ctttatgtgt tcttactcgg cctcatagtg gtgtattaac      300
tgccatagat caagctttaa tgacctgtga gatgttaaag gaatatcctg aaaagtgtac      360
ggaagaacag attcgatcat tattggctgc agatcatcca gaagtgcagg tagctacttt      420
acagatcatt ctgagaggag gttagagtatt ccggtcatct tctataattg aatcggttct      480
cgtgccgnt

```

<210> 288

<211> 191

<212> DNA

<213> Chlamydia

```

<400> 288
ggatccgaat tcaggatgat ctgttgggtt atcaataaaa aggggtttgc ctttttttaa      60
gacgactttg tagataacgc taggagctgt agcaataata tcgagatcaa attctctaga      120
gattctctca aagatgattt ctaagtgcag cagtccataa aatccacagc ggaacccaaa      180
tcggagagag t

```

<210> 289

<211> 515

<212> DNA

<213> Chlamydia

```

<400> 289
ggatccgaat tcggcacgag gagcgacgtg aaatagtga atcttcccgat attcttatta      60
cttctcggtt gccttacgca aatgggtcctt tgcatttttg acatattacc ggtgcttatt      120
tgccctcgag tgtttatgcg cgttttcaga gactacaagg caaagaggtt ttgtatattt      180
gtggttctga tgaatacggg atcgcaatta ccttaaatgc agagtgggca ggcattgggt      240
atcaagaata tgcgcacatg tatcataaagc ttcataaaga taccttcaag aaattgggaa      300
tttctgtaga tttcttttcc agaactacga acgcttatca tctctctatt gtgcaagatt      360
tctatcgaaa cttgcaggaa ccgggactcg tagagaatca ggtgaccgaa cagctgtatt      420
ctgaggaaga agggaaagtt ttgacggacc gttatgttgt aggtacttgt cccaagtgtg      480
ggtttgatcg agctcgagga gatgagtgtc agcag

```

<210> 290

<211> 522

<212> DNA

<213> Chlamydia

```

<400> 290
ggatccgaat tcggcacgag ggaggaatgg aagggccctc cgattktama tctgctacca      60
tgcatctcac tagaaaactc ataacacggg ttttctctga tggcgagtaa gaagcaagca      120
tttgatgtaa attagcgcaa ttgagggggg atgaggttac ttggaaatat aaggagcgaa      180
gcgatgaagg agatgtattt gctctgggaag caaagggttc tgaagctaac agaacattgc      240
gtcctccaaac aatcgctctga ggattctgccc tcatcagttg atgctttggc tgaatgagag      300
cggacttaag tttccatca gagggagcta tttgaattag ataataaaga gctagatcct      360
ttattgtggg atcagaaaaa ttacttgtga gcgcacgag aatttcgtca gaagaagaat      420
catcatcgaa cgaatttttc aatcctcgaa aatcttctcc agagacttcg gaaagatctt      480
ctgtgaaacg atcttcaaga ggagtatgc ctttttcocg tg

```

<210> 291

<211> 1002

<212> DNA

<213> Chlamydia

<400> 291

```

atggcgacta acgcaattag atcggcagga agtcgacgaa gtaagatgct gctgccagtt      60
gccaaagaac cagcggctgt cagctccttt gctcagaaag ggattattgt tattcaacaa      120
ttttttacaa accctgggaa taagttagca aagttttagt gggcaacaaa aagtttagat      180
aaatgcttta agctaagtaa ggcggtttct gactgtgtcg taggatcgct ggaagaggcg      240
ggatgcacag gggacgcatt gacctccgcg agaaacgccc agggtagtgt aaaaacaact      300
cgagaagttg ttgccttagc taatgtgtct aatggagctg ttccatctat cgtttaactcg      360
actcagaggt gttaccaata cacacgtcaa gccttcgagt taggaagcaa gacaaaagaa      420
agaaaaacgc ctggggagta tagtaaaatg ctattaactc gaggtgatta cctattggca      480
gcttcacagg aagcttgtac ggccagtcgt gcaacgactt actcagcgac attcgtgtgt      540
ttacgtccgt taatgttaat caataaaact acagcaaac cattcttaga caaagcgact      600
gtaggcaatt ttggcaccgc tgttgctgga attatgacca ttaatcatat ggcaggagtt      660
gctggtgctg ttggcggaat cgcattagaa caaaagctgt tcaaacgtgc gaaggaaatcc      720
ctatacaatg agagatgtgc cttagaaaaa caacaatctc agttgagtg ggcagtgatt      780
ctaagcgcgc aaagggcatt acgtaaagaa cacgttgcta ctctaaaaag aaatgtttta      840
actctctctg aaaaagcttt agagtttgta gtggatggag tcaaaactcat tcctttaccg      900
attacagtgg cttgctccgc tgcaatttct ggagccttga cgcgacgac cgcaggaatt      960
ggcttatata gcatatggca gaaaacaaag tctggcgaat aa      1002

```

<210> 292

<211> 333

<212> PRT

<213> Chlamydia

<400> 292

```

Met Ala Thr Asn Ala Ile Arg Ser Ala Gly Ser Ala Ala Ser Lys Met
1          5          10          15
Leu Leu Pro Val Ala Lys Glu Pro Ala Ala Val Ser Ser Phe Ala Gln
20          25          30
Lys Gly Ile Tyr Cys Ile Gln Gln Phe Phe Thr Asn Pro Gly Asn Lys
35          40          45
Leu Ala Lys Phe Val Gly Ala Thr Lys Ser Leu Asp Lys Cys Phe Lys
50          55          60
Leu Ser Lys Ala Val Ser Asp Cys Val Val Gly Ser Leu Glu Glu Ala
65          70          75          80
Gly Cys Thr Gly Asp Ala Leu Thr Ser Ala Arg Asn Ala Gln Gly Met
85          90          95
Leu Lys Thr Thr Arg Glu Val Val Ala Leu Ala Asn Val Leu Asn Gly
100         105         110
Ala Val Pro Ser Ile Val Asn Ser Thr Gln Arg Cys Thr Gln Tyr Thr
115         120         125
Arg Gln Ala Phe Glu Leu Gly Ser Lys Thr Lys Glu Arg Lys Thr Pro
130         135         140
Gly Glu Tyr Ser Lys Met Leu Leu Thr Arg Gly Asp Tyr Leu Leu Ala
145         150         155         160
Ala Ser Arg Glu Ala Cys Thr Ala Val Gly Ala Thr Thr Tyr Ser Ala
165         170         175
Thr Phe Gly Val Leu Arg Pro Leu Met Leu Ile Asn Lys Leu Thr Ala
180         185         190
Lys Pro Phe Leu Asp Lys Ala Thr Val Gly Asn Phe Gly Thr Ala Val
195         200         205
Ala Gly Ile Met Thr Ile Asn His Met Ala Gly Val Ala Gly Ala Val
210         215         220
Gly Gly Ile Ala Leu Glu Gln Lys Leu Phe Lys Arg Ala Lys Glu Ser

```

```

225          230          235          240
Leu Tyr Asn Glu Arg Cys Ala Leu Glu Asn Gln Gln Ser Gln Leu Ser
          245          250          255
Gly Asp Val Ile Leu Ser Ala Glu Arg Ala Leu Arg Lys Glu His Val
          260          265          270
Ala Thr Leu Lys Arg Asn Val Leu Thr Leu Leu Glu Lys Ala Leu Glu
          275          280          285
Leu Val Val Asp Gly Val Lys Leu Ile Pro Leu Pro Ile Thr Val Ala
          290          295          300
Cys Ser Ala Ala Ile Ser Gly Ala Leu Thr Ala Ala Ser Ala Gly Ile
          305          310          315          320
Gly Leu Tyr Ser Ile Trp Gln Lys Thr Lys Ser Gly Lys
          325          330

```

<210> 293

<211> 7

<212> DNA

<213> Chlamydia

<400> 293

tgcaatc

7

<210> 294

<211> 196

<212> PRT

<213> Chlamydia

<400> 294

```

Thr Met Gly Ser Leu Val Gly Arg Gln Ala Pro Asp Phe Ser Gly Lys
          5          10          15

```

```

Ala Val Val Cys Gly Glu Glu Lys Glu Ile Ser Leu Ala Asp Phe Arg
          20          25          30

```

```

Gly Lys Tyr Val Val Leu Phe Phe Tyr Pro Lys Asp Phe Thr Tyr Val
          35          40          45

```

```

Cys Pro Thr Glu Leu His Ala Phe Gln Asp Arg Leu Val Asp Phe Glu
          50          55          60

```

```

Glu His Gly Ala Val Val Leu Gly Cys Ser Val Asp Asp Ile Glu Thr
          65          70          75          80

```

```

His Ser Arg Trp Leu Thr Val Ala Arg Asp Ala Gly Gly Ile Glu Gly
          85          90          95

```

```

Thr Glu Tyr Pro Leu Leu Ala Asp Pro Ser Phe Lys Ile Ser Glu Ala
          100          105          110

```

```

Phe Gly Val Leu Asn Pro Glu Gly Ser Leu Ala Leu Arg Ala Thr Phe
          115          120          125

```

```

Leu Ile Asp Lys His Gly Val Ile Arg His Ala Val Ile Asn Asp Leu
          130          135          140

```

```

Pro Leu Gly Arg Ser Ile Asp Glu Glu Leu Arg Ile Leu Asp Ser Leu
          145          150          155          160

```

Ile Phe Phe Glu Asn His Gly Met Val Cys Pro Ala Asn Trp Arg Ser
 165 170 175

Gly Glu Arg Gly Met Val Pro Ser Glu Gly Leu Lys Glu Tyr Phe
 180 185 190

Gln Thr Met Asp
 195

<210> 295
 <211> 181
 <212> PRT
 <213> Chlamydia

<400> 295
 Lys Gly Gly Lys Met Ser Thr Thr Ile Ser Gly Asp Ala Ser Ser Leu
 5 10 15

Pro Leu Pro Thr Ala Ser Cys Val Glu Thr Lys Ser Thr Ser Ser Ser
 20 25 30

Thr Lys Gly Asn Thr Cys Ser Lys Ile Leu Asp Ile Ala Leu Ala Ile
 35 40 45

Val Gly Ala Leu Val Val Val Ala Gly Val Leu Ala Leu Val Leu Cys
 50 55 60

Ala Ser Asn Val Ile Phe Thr Val Ile Gly Ile Pro Ala Leu Ile Ile
 65 70 75 80

Gly Ser Ala Cys Val Gly Ala Gly Ile Ser Arg Leu Met Tyr Arg Ser
 85 90 95

Ser Tyr Ala Ser Leu Glu Ala Lys Asn Val Leu Ala Glu Gln Arg Leu
 100 105 110

Arg Asn Leu Ser Glu Glu Lys Asp Ala Leu Ala Ser Val Ser Phe Ile
 115 120 125

Asn Lys Met Phe Leu Arg Gly Leu Thr Asp Asp Leu Gln Ala Leu Glu
 130 135 140

Ala Lys Val Met Glu Phe Glu Ile Asp Cys Leu Asp Arg Leu Glu Lys
 145 150 155 160

Asn Glu Gln Ala Leu Leu Ser Asp Val Arg Leu Val Leu Ser Ser Tyr
 165 170 175

Thr Arg Trp Leu Asp
 180

<210> 296
 <211> 124
 <212> PRT
 <213> Chlamydia

<400> 296

```

Ile Tyr Glu Val Met Asn Met Asp Leu Glu Thr Arg Arg Ser Phe Ala
      5                      10                      15

Val Gln Gln Gly His Tyr Gln Asp Pro Arg Ala Ser Asp Tyr Asp Leu
      20                      25                      30

Pro Arg Ala Ser Asp Tyr Asp Leu Pro Arg Ser Pro Tyr Pro Thr Pro
      35                      40                      45

Pro Leu Pro Ser Pro Arg Tyr Gln Leu Gln Asn Met Asp Val Glu Ala Gly
      50                      55                      60

Phe Arg Glu Ala Val Tyr Ala Ser Phe Val Ala Gly Met Tyr Asn Tyr
      65                      70                      75                      80

Val Val Thr Gln Pro Gln Glu Arg Ile Pro Asn Ser Gln Gln Val Glu
      85                      90                      95

Gly Ile Leu Arg Asp Met Leu Thr Asn Gly Ser Gln Thr Phe Ser Asn
      100                     105                     110

Leu Met Gln Arg Trp Asp Arg Glu Val Asp Arg Glu
      115                     120

```

<210> 297

<211> 488

<212> PRT

<213> Chlamydia

<400> 297

```

Lys Gly Ser Leu Pro Ile Leu Gly Pro Phe Leu Asn Gly Lys Met Gly
      5                      10                      15

Phe Trp Arg Thr Ser Ile Met Lys Met Asn Arg Ile Trp Leu Leu Leu
      20                      25                      30

Leu Thr Phe Ser Ser Ala Ile His Ser Pro Val Arg Gly Glu Ser Leu
      35                      40                      45

Val Cys Lys Asn Ala Leu Gln Asp Leu Ser Phe Leu Glu His Leu Leu
      50                      55                      60

Gln Val Lys Tyr Ala Pro Lys Thr Trp Lys Glu Gln Tyr Leu Gly Trp
      65                      70                      75                      80

Asp Leu Val Gln Ser Ser Val Ser Ala Gln Gln Lys Leu Arg Thr Gln
      85                      90                      95

Glu Asn Pro Ser Thr Ser Phe Cys Gln Gln Val Leu Ala Asp Phe Ile
      100                     105                     110

Gly Gly Leu Asn Asp Phe His Ala Gly Val Thr Phe Phe Ala Ile Glu
      115                     120                     125

Ser Ala Tyr Leu Pro Tyr Thr Val Gln Lys Ser Ser Asp Gly Arg Phe
      130                     135                     140

```

Tyr Phe Val Asp Ile Met Thr Phe Ser Ser Glu Ile Arg Val Gly Asp
 145 150 155 160
 Glu Leu Leu Glu Val Asp Gly Ala Pro Val Gln Asp Val Leu Ala Thr
 165 170 175
 Leu Tyr Gly Ser Asn His Lys Gly Thr Ala Ala Glu Glu Ser Ala Ala
 180 185 190
 Leu Arg Thr Leu Phe Ser Arg Met Ala Ser Leu Gly His Lys Val Pro
 195 200 205
 Ser Gly Arg Thr Thr Leu Lys Ile Arg Arg Pro Phe Gly Thr Thr Arg
 210 215 220
 Glu Val Arg Val Lys Trp Arg Tyr Val Pro Glu Gly Val Gly Asp Leu
 225 230 235 240
 Ala Thr Ile Ala Pro Ser Ile Arg Ala Pro Gln Leu Gln Lys Ser Met
 245 250 255
 Arg Ser Phe Phe Pro Lys Lys Asp Asp Ala Phe His Arg Ser Ser Ser
 260 265 270
 Leu Phe Tyr Ser Pro Met Val Pro His Phe Trp Ala Glu Leu Arg Asn
 275 280 285
 His Tyr Ala Thr Ser Gly Leu Lys Ser Gly Tyr Asn Ile Gly Ser Thr
 290 295 300
 Asp Gly Phe Leu Pro Val Ile Gly Pro Val Ile Trp Glu Ser Glu Gly
 305 310 315 320
 Leu Phe Arg Ala Tyr Ile Ser Ser Val Thr Asp Gly Asp Gly Lys Ser
 325 330 335
 His Lys Val Gly Phe Leu Arg Ile Pro Thr Tyr Ser Trp Gln Asp Met
 340 345 350
 Glu Asp Phe Asp Pro Ser Gly Pro Pro Pro Trp Glu Glu Phe Ala Lys
 355 360 365
 Ile Ile Gln Val Phe Ser Ser Asn Thr Glu Ala Leu Ile Ile Asp Gln
 370 375 380
 Thr Asn Asn Pro Gly Gly Ser Val Leu Tyr Leu Tyr Ala Leu Leu Ser
 385 390 395 400
 Met Leu Thr Asp Arg Pro Leu Glu Leu Pro Lys His Arg Met Ile Leu
 405 410 415
 Thr Gln Asp Glu Val Val Asp Ala Leu Asp Trp Leu Thr Leu Leu Glu
 420 425 430
 Asn Val Asp Thr Asn Val Glu Ser Arg Leu Ala Leu Gly Asp Asn Met
 435 440 445

Glu Gly Tyr Thr Val Asp Leu Gln Val Ala Glu Tyr Leu Lys Ser Phe
 450 455 460

Gly Arg Gln Val Leu Asn Cys Trp Ser Lys Gly Asp Ile Glu Leu Ser
 465 470 475 480

Thr Pro Ile Pro Leu Phe Gly Phe
 485

<210> 298
 <211> 140
 <212> PRT
 <213> Chlamydia

<400> 298
 Arg Ile Asp Ile Ser Ser Val Thr Phe Phe Ile Gly Ile Leu Leu Ala
 5 10 15

Val Asn Ala Leu Thr Tyr Ser His Val Leu Arg Asp Leu Ser Val Ser
 20 25 30

Met Asp Ala Leu Phe Ser Arg Asn Thr Leu Ala Val Leu Leu Gly Leu
 35 40 45

Val Ser Ser Val Leu Asp Asn Val Pro Leu Val Ala Ala Thr Ile Gly
 50 55 60

Met Tyr Asp Leu Pro Met Asn Asp Pro Leu Trp Lys Leu Ile Ala Tyr
 65 70 75 80

Thr Ala Gly Thr Gly Gly Ser Ile Leu Ile Ile Gly Ser Ala Ala Gly
 85 90 95

Val Ala Tyr Met Gly Met Glu Lys Val Ser Phe Gly Trp Tyr Val Lys
 100 105 110

His Ala Ser Trp Ile Ala Leu Ala Ser Tyr Phe Gly Gly Leu Ala Val
 115 120 125

Tyr Phe Leu Met Glu Asn Cys Val Asn Leu Phe Val
 130 135 140

<210> 299
 <211> 361
 <212> PRT
 <213> Chlamydia

<400> 299
 His Gln Glu Ile Ala Asp Ser Pro Leu Val Lys Lys Ala Glu Glu Gln
 5 10 15

Ile Asn Gln Ala Gln Gln Asp Ile Gln Thr Ile Thr Pro Ser Gly Leu
 20 25 30

Asp Ile Pro Ile Val Gly Pro Ser Gly Ser Ala Ala Ser Ala Gly Ser
 35 40 45

Ala Ala Gly Ala Leu Lys Ser Ser Asn Asn Ser Gly Arg Ile Ser Leu
 50 55 60
 Leu Leu Asp Asp Val Asp Asn Glu Met Ala Ala Ile Ala Met Gln Gly
 65 70 75 80
 Phe Arg Ser Met Ile Glu Gln Phe Asn Val Asn Asn Pro Ala Thr Ala
 85 90 95
 Lys Glu Leu Gln Ala Met Glu Ala Gln Leu Thr Ala Met Ser Asp Gln
 100 105 110
 Leu Val Gly Ala Asp Gly Glu Leu Pro Ala Glu Ile Gln Ala Ile Lys
 115 120 125
 Asp Ala Leu Ala Gln Ala Leu Lys Gln Pro Ser Ala Asp Gly Leu Ala
 130 135 140
 Thr Ala Met Gly Gln Val Ala Phe Ala Ala Lys Val Gly Gly Gly
 145 150 155 160
 Ser Ala Gly Thr Ala Gly Thr Val Gln Met Asn Val Lys Gln Leu Tyr
 165 170 175
 Lys Thr Ala Phe Ser Ser Thr Ser Ser Ser Tyr Ala Ala Ala Leu
 180 185 190
 Ser Asp Gly Tyr Ser Ala Tyr Lys Thr Leu Asn Ser Leu Tyr Ser Glu
 195 200 205
 Ser Arg Ser Gly Val Gln Ser Ala Ile Ser Gln Thr Ala Asn Pro Ala
 210 215 220
 Leu Ser Arg Ser Val Ser Arg Ser Gly Ile Glu Ser Gln Gly Arg Ser
 225 230 235 240
 Ala Asp Ala Ser Gln Arg Ala Ala Glu Thr Ile Val Arg Asp Ser Gln
 245 250 255
 Thr Leu Gly Asp Val Tyr Ser Arg Leu Gln Val Leu Asp Ser Leu Met
 260 265 270
 Ser Thr Ile Val Ser Asn Pro Gln Ala Asn Gln Glu Glu Ile Met Gln
 275 280 285
 Lys Leu Thr Ala Ser Ile Ser Lys Ala Pro Gln Phe Gly Tyr Pro Ala
 290 295 300
 Val Gln Asn Ser Val Asp Ser Leu Gln Lys Phe Ala Ala Gln Leu Glu
 305 310 315 320
 Arg Glu Phe Val Asp Gly Glu Arg Ser Leu Ala Glu Ser Gln Glu Asn
 325 330 335
 Ala Phe Arg Lys Gln Pro Ala Phe Ile Gln Gln Val Leu Val Asn Ile
 340 345 350

Ala Ser Leu Phe Ser Gly Tyr Leu Ser
355 360

<210> 300
<211> 207
<212> PRT
<213> Chlamydia

<400> 300
Ser Ser Lys Ile Val Ser Leu Cys Glu Gly Ala Val Ala Asp Ala Arg
5 10 15
Met Cys Lys Ala Glu Leu Ile Lys Lys Glu Ala Asp Ala Tyr Leu Phe
20 25 30
Cys Glu Lys Ser Gly Ile Tyr Leu Thr Lys Lys Glu Gly Ile Leu Ile
35 40 45
Pro Ser Ala Gly Ile Asp Glu Ser Asn Thr Asp Gln Pro Phe Val Leu
50 55 60
Tyr Pro Lys Asp Ile Leu Gly Ser Cys Asn Arg Ile Gly Glu Trp Leu
65 70 75 80
Arg Asn Tyr Phe Arg Val Lys Glu Leu Gly Val Ile Ile Thr Asp Ser
85 90 95
His Thr Thr Pro Met Arg Arg Gly Val Leu Gly Ile Gly Leu Cys Trp
100 105 110
Tyr Gly Phe Ser Pro Leu His Asn Tyr Ile Gly Ser Leu Asp Cys Phe
115 120 125
Gly Arg Pro Leu Gln Met Thr Gln Ser Asn Leu Val Asp Ala Leu Ala
130 135 140
Val Ala Ala Val Val Cys Met Gly Glu Gly Asn Glu Gln Thr Pro Leu
145 150 155 160
Ala Val Ile Glu Gln Ala Pro Asn Met Val Tyr His Ser Tyr Pro Thr
165 170 175
Ser Arg Glu Glu Tyr Cys Ser Leu Arg Ile Asp Glu Thr Glu Asp Leu
180 185 190
Tyr Gly Pro Phe Leu Gln Ala Val Thr Trp Ser Gln Glu Lys Lys
195 200 205

<210> 301
<211> 183
<212> PRT
<213> Chlamydia

<400> 301
Ile Pro Pro Ala Pro Arg Gly His Pro Gln Ile Glu Val Thr Phe Asp
5 10 15

Ile Asp Ala Asn Gly Ile Leu His Val Ser Ala Lys Asp Ala Ala Ser
 20 25 30
 Gly Arg Glu Gln Lys Ile Arg Ile Glu Ala Ser Ser Gly Leu Lys Glu
 35 40 45
 Asp Glu Ile Gln Gln Met Ile Arg Asp Ala Glu Leu His Lys Glu Glu
 50 55 60
 Asp Lys Gln Arg Lys Glu Ala Ser Asp Val Lys Asn Glu Ala Asp Gly
 65 70 75 80
 Met Ile Phe Arg Ala Glu Lys Ala Val Lys Asp Tyr His Asp Lys Ile
 85 90 95
 Pro Ala Glu Leu Val Lys Glu Ile Glu Glu His Ile Glu Lys Val Arg
 100 105 110
 Gln Ala Ile Lys Glu Asp Ala Ser Thr Thr Ala Ile Lys Ala Ala Ser
 115 120 125
 Asp Glu Leu Ser Thr Arg Met Gln Lys Ile Gly Glu Ala Met Gln Ala
 130 135 140
 Gln Ser Ala Ser Ala Ala Ala Ser Ser Ala Ala Asn Ala Gln Gly Gly
 145 150 155 160
 Pro Asn Ile Asn Ser Glu Asp Leu Lys Lys His Ser Phe Ser Thr Arg
 165 170 175
 Pro Pro Ala Gly Gly Ser Ala
 180

<210> 302

<211> 232

<212> PRT

<213> Chlamydia

<400> 302

Met Thr Lys His Gly Lys Arg Ile Arg Gly Ile Gln Glu Thr Tyr Asp
 5 10 15
 Leu Ala Lys Ser Tyr Ser Leu Gly Glu Ala Ile Asp Ile Leu Lys Gln
 20 25 30
 Cys Pro Thr Val Arg Phe Asp Gln Thr Val Asp Val Ser Val Lys Leu
 35 40 45
 Gly Ile Asp Pro Arg Lys Ser Asp Gln Gln Ile Arg Gly Ser Val Ser
 50 55 60
 Leu Pro His Gly Thr Gly Lys Val Leu Arg Ile Leu Val Phe Ala Ala
 65 70 75 80
 Gly Asp Lys Ala Ala Glu Ala Ile Glu Ala Gly Ala Asp Phe Val Gly
 85 90 95

Ser Asp Asp Leu Val Glu Lys Ile Lys Gly Gly Trp Val Asp Phe Asp
 100 105 110
 Val Ala Val Ala Thr Pro Asp Met Met Arg Glu Val Gly Lys Leu Gly
 115 120 125
 Lys Val Leu Gly Pro Arg Asn Leu Met Pro Thr Pro Lys Ala Gly Thr
 130 135 140
 Val Thr Thr Asp Val Val Lys Thr Ile Ala Glu Leu Arg Lys Gly Lys
 145 150 155 160
 Ile Glu Phe Lys Ala Asp Arg Ala Gly Val Cys Asn Val Gly Val Ala
 165 170 175
 Lys Leu Ser Phe Asp Ser Ala Gln Ile Lys Glu Asn Val Glu Ala Leu
 180 185 190
 Cys Ala Ala Leu Val Lys Ala Lys Pro Ala Thr Ala Lys Gly Gln Tyr
 195 200 205
 Leu Val Asn Phe Thr Ile Ser Ser Thr Met Gly Pro Gly Val Thr Val
 210 215 220
 Asp Thr Arg Glu Leu Ile Ala Leu
 225 230

 <210> 303
 <211> 238
 <212> PRT
 <213> chlamydia

 <400> 303
 Ile Asn Ser Lys Leu Glu Thr Lys Asn Leu Ile Tyr Leu Lys Leu Lys
 5 10 15
 Ile Lys Lys Ser Phe Lys Met Gly Asn Ser Gly Phe Tyr Leu Tyr Asn
 20 25 30
 Thr Gln Asn Cys Val Phe Ala Asp Asn Ile Lys Val Gly Gln Met Thr
 35 40 45
 Glu Pro Leu Lys Asp Gln Gln Ile Ile Leu Gly Thr Thr Ser Thr Pro
 50 55 60
 Val Ala Ala Lys Met Thr Ala Ser Asp Gly Ile Ser Leu Thr Val Ser
 65 70 75 80
 Asn Asn Pro Ser Thr Asn Ala Ser Ile Thr Ile Gly Leu Asp Ala Gly
 85 90 95
 Lys Ala Tyr Gln Leu Ile Leu Glu Lys Leu Gly Asp Gln Ile Leu Gly
 100 105 110
 Gly Ile Ala Asp Thr Ile Val Asp Ser Thr Val Gln Asp Ile Leu Asp
 115 120 125

Lys Ile Thr Thr Asp Pro Ser Leu Gly Leu Leu Lys Ala Phe Asn Asn
 130 135 140
 Phe Pro Ile Thr Asn Lys Ile Gln Cys Asn Gly Leu Phe Thr Pro Arg
 145 150 155 160
 Asn Ile Glu Thr Leu Leu Gly Gly Thr Glu Ile Gly Lys Phe Thr Val
 165 170 175
 Thr Pro Lys Ser Ser Gly Ser Met Phe Leu Val Ser Ala Asp Ile Ile
 180 185 190
 Ala Ser Arg Met Glu Gly Gly Val Val Leu Ala Leu Val Arg Glu Gly
 195 200 205
 Asp Ser Lys Pro Tyr Ala Ile Ser Tyr Gly Tyr Ser Ser Gly Val Pro
 210 215 220
 Asn Leu Cys Ser Leu Arg Thr Arg Ile Ile Asn Thr Gly Leu
 225 230 235
 <210> 304
 <211> 133
 <212> PRT
 <213> Chlamydia
 <400> 304
 His Met His His His His His Met Ala Ser Ile Cys Gly Arg Leu
 5 10 15
 Gly Ser Gly Thr Gly Asn Ala Leu Lys Ala Phe Phe Thr Gln Pro Ser
 20 25 30
 Asn Lys Met Ala Arg Val Val Asn Lys Thr Lys Gly Met Asp Lys Thr
 35 40 45
 Val Lys Val Ala Lys Ser Ala Ala Glu Leu Thr Ala Asn Ile Leu Glu
 50 55 60
 Gln Ala Gly Gly Ala Gly Ser Ser Ala His Ile Thr Ala Ser Gln Val
 65 70 75 80
 Ser Lys Gly Leu Gly Asp Thr Arg Thr Val Val Ala Leu Gly Asn Ala
 85 90 95
 Phe Asn Gly Ala Leu Pro Gly Thr Val Gln Ser Ala Gln Ser Phe Phe
 100 105 110
 Ser His Met Lys Ala Ala Ser Gln Lys Thr Gln Glu Gly Asp Glu Gly
 115 120 125
 Leu Thr Ala Asp Leu
 130

<210> 305

<211> 125

<212> PRT

<213> Chlamydia

<400> 305

Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
 5 10 15

Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn
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Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
 35 40 45

Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
 50 55 60

Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Thr Arg
 65 70 75 80

Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
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Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
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Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu
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<210> 306

<211> 38

<212> DNA

<213> Chlamydia trachomatis

<400> 306

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<210> 307

<211> 39

<212> DNA

<213> Chlamydia trachomatis

<400> 307

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<210> 308

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<212> DNA

<213> Chlamydia trachomatis

<400> 308

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<210> 309

<211> 619

<212> PRT

<213> Chlamydia trachomatis

<400> 309

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Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
35 40 45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
50 55 60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65 70 75 80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
85 90 95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
100 105 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
115 120 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
130 135 140
Arg Pro Leu Met Phe Ile Thr Lys Glu Leu Met Asn Arg Val Ile Glu
145 150 155 160
Ile His Ala His Tyr Asp Gln Arg Gln Leu Ser Gln Ser Pro Asn Thr
165 170 175
Asn Phe Leu Val His His Pro Tyr Leu Thr Leu Ile Pro Lys Phe Leu
180 185 190
Leu Gly Ala Leu Ile Val Tyr Ala Pro Tyr Ser Phe Ala Glu Met Glu
195 200 205

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Leu Ala Ile Ser Gly His Lys Gln Gly Lys Asp Arg Asp Thr Phe Thr
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 Met Ile Ser Ser Cys Pro Glu Gly Thr Asn Tyr Ile Ile Asn Arg Lys
 225 230 235 240
 Leu Ile Leu Ser Asp Phe Ser Leu Leu Asn Lys Val Ser Ser Gly Gly
 245 250 255
 Ala Phe Arg Asn Leu Ala Gly Lys Ile Ser Phe Leu Gly Lys Asn Ser
 260 265 270
 Ser Ala Ser Ile His Phe Lys His Ile Asn Ile Asn Gly Phe Gly Ala
 275 280 285
 Gly Val Phe Ser Glu Ser Ser Ile Glu Phe Thr Asp Leu Arg Lys Leu
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 Val Ala Phe Gly Ser Glu Ser Thr Gly Gly Ile Phe Thr Ala Lys Glu
 305 310 315 320
 Asp Ile Ser Phe Lys Asn Asn His His Ile Ala Phe Arg Asn Asn Ile
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 Thr Lys Gly Asn Gly Gly Val Ile Gln Leu Gln Gly Asp Met Lys Gly
 340 345 350
 Ser Val Ser Phe Val Asp Gln Arg Gly Ala Ile Ile Phe Thr Asn Asn
 355 360 365
 Gln Ala Val Thr Ser Ser Ser Met Lys His Ser Gly Arg Gly Gly Ala
 370 375 380
 Ile Ser Gly Asp Phe Ala Gly Ser Arg Ile Leu Phe Leu Asn Asn Gln
 385 390 395 400
 Gln Ile Thr Phe Glu Gly Asn Ser Ala Val His Gly Gly Ala Ile Tyr
 405 410 415
 Asn Lys Asn Gly Leu Val Glu Phe Leu Gly Asn Ala Gly Pro Leu Ala
 420 425 430
 Phe Lys Glu Asn Thr Thr Ile Ala Asn Gly Gly Ala Ile Tyr Thr Ser
 435 440 445
 Asn Phe Lys Ala Asn Gln Gln Thr Ser Pro Ile Leu Phe Ser Gln Asn
 450 455 460
 His Ala Asn Lys Lys Gly Gly Ala Ile Tyr Ala Gln Tyr Val Asn Leu
 465 470 475 480
 Glu Gln Asn Gln Asp Thr Ile Arg Phe Glu Lys Asn Thr Ala Lys Glu
 485 490 495
 Gly Gly Gly Ala Ile Thr Ser Ser Gln Cys Ser Ile Thr Ala His Asn
 500 505 510
 Thr Ile Thr Phe Ser Asp Asn Ala Ala Gly Asp Leu Gly Gly Gly Ala
 515 520 525
 Ile Leu Leu Glu Gly Lys Lys Pro Ser Leu Thr Leu Ile Ala His Ser
 530 535 540
 Gly Asn Ile Ala Phe Ser Gly Asn Thr Met Leu His Ile Thr Lys Lys
 545 550 555 560
 Ala Ser Leu Asp Arg His Asn Ser Ile Leu Ile Lys Glu Ala Pro Tyr
 565 570 575
 Lys Ile Gln Leu Ala Ala Asn Lys Asn His Ser Ile His Phe Phe Asp
 580 585 590
 Pro Val Met Ala Leu Ser Ala Ser Ser Pro Ile Gln Ile Asn Ala
 595 600 605
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<211> 39

<212> DNA

<213> Chlamydia trachomatis

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acgcttcata tccgggctac cgccttctct ggcttgggtg ttgtcgacaa caacggcaac	180
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<212> PRT	
<213> Chlamydia trachomatis	

<400> 313

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Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
 35          40          45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
 50          55          60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
 65          70          75          80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
 85          90          95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
100          105          110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
115          120          125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
130          135          140
Arg Pro Leu His Ser Ile His Phe Phe Asp Pro Val Met Ala Leu Ser
145          150          155          160
Ala Ser Ser Ser Pro Ile Gln Ile Asn Ala Pro Glu Tyr Glu Thr Pro
165          170          175
Phe Phe Ser Pro Lys Gly Met Ile Val Phe Ser Gly Ala Asn Leu Leu
180          185          190
Asp Asp Ala Arg Glu Asp Val Ala Asn Arg Thr Ser Ile Phe Asn Gln
195          200          205
Pro Val His Leu Tyr Asn Gly Thr Leu Ser Ile Glu Asn Gly Ala His
210          215          220
Leu Ile Val Gln Ser Phe Lys Gln Thr Gly Gly Arg Ile Ser Leu Ser
225          230          235          240
Pro Gly Ser Ser Leu Ala Leu Tyr Thr Met Asn Ser Phe Phe His Gly
245          250          255
Asn Ile Ser Ser Lys Glu Pro Leu Glu Ile Asn Gly Leu Ser Phe Gly
260          265          270
Val Asp Ile Ser Pro Ser Asn Leu Gln Ala Glu Ile Arg Ala Gly Asn
275          280          285
Ala Pro Leu Arg Leu Ser Gly Ser Pro Ser Ile His Asp Pro Glu Gly
290          295          300
Leu Phe Tyr Glu Asn Arg Asp Thr Ala Ala Ser Pro Tyr Gln Met Glu
305          310          315          320
Ile Leu Leu Thr Ser Asp Lys Thr Val Asp Ile Ser Lys Phe Thr Thr
325          330          335
Asp Ser Leu Val Thr Asn Lys Gln Ser Gly Phe Gln Gly Ala Trp His
340          345          350
Phe Ser Trp Gln Pro Asn Thr Ile Asn Asn Thr Lys Gln Lys Ile Leu
355          360          365
Arg Ala Ser Trp Leu Pro Thr Gly Glu Tyr Val Leu Glu Ser Asn Arg
370          375          380
Val Gly Arg Ala Val Pro Asn Ser Leu Trp Ser Thr Phe Leu Leu Leu
385          390          395          400
Gln Thr Ala Ser His Asn Leu Gly Asp His Leu Cys Asn Asn Arg Ser
405          410          415
Leu Ile Pro Thr Ser Tyr Phe Gly Val Leu Ile Gly Gly Thr Gly Ala
420          425          430
Glu Met Ser Thr His Ser Ser Glu Glu Glu Ser Phe Ile Ser Arg Leu
435          440          445
Gly Ala Thr Gly Thr Ser Ile Ile Arg Leu Thr Pro Ser Leu Thr Leu

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450 455 460
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 465 470 475 480
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 485 490 495
 His Val Trp Gly Pro Leu Thr Val Asn Ser Thr Leu Cys Ala Ala Leu
 500 505 510
 Asp His Asn Ala Met Val Arg Ile Cys Ser Lys Lys Asp His Thr Tyr
 515 520 525
 Gly Lys Trp Asp Thr Phe Gly Met Arg Gly Thr Leu Gly Ala Ser Tyr
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 Thr Phe Leu Glu Tyr Asp Gln Thr Met Arg Val Phe Ser Phe Ala Asn
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 Ile Glu Ala Thr Asn Ile Leu Gln Arg Ala Phe Thr Glu Thr Gly Tyr
 565 570 575
 Asn Pro Arg Ser Phe Ser Lys Thr Lys Leu Asn Ile Ala Ile Pro
 580 585 590
 Ile Gly Ile Gly Tyr Glu Phe Cys Leu Gly Asn Ser Ser Phe Ala Leu
 595 600 605
 Leu Gly Lys Gly Ser Ile Gly Tyr Ser Arg Asp Ile Lys Arg Glu Asn
 610 615 620
 Pro Ser Thr Leu Ala His Leu Ala Met Asn Asp Phe Ala Trp Thr Thr
 625 630 635 640
 Asn Gly Cys Ser Val Pro Thr Ser Ala His Thr Leu Ala Asn Gln Leu
 645 650 655
 Ile Leu Arg Tyr Lys Ala Cys Ser Leu Tyr Ile Thr Ala Tyr Thr Ile
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 Val Gly Phe
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<210> 314

<211> 38

<212> DNA

<213> Chlamydia trachomatis

<400> 314

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38

<210> 315

<211> 36

<212> DNA

<213> Chlamydia trachomatis

<400> 315

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36

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<211> 1941

<212> DNA

<213> Chlamydia trachomatis

<400> 316

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 gggcacagag tccaacgcgt ggtcgggagc gtcgggcgcg caagtctcgg catctccacc 240

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<210> 317

<211> 646

<212> PRT

<213> Chlamydia trachomatis

<400> 317

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35 40 45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
50 55 60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65 70 75 80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
85 90 95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
100 105 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
115 120 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
130 135 140
Arg Pro Leu Met Ile Lys Arg Thr Ser Leu Ser Phe Ala Cys Leu Ser
145 150 155 160
Phe Phe Tyr Leu Ser Thr Ile Ser Ile Leu Gln Ala Asn Glu Thr Asp
165 170 175

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Thr Leu Gln Phe Arg Arg Phe Thr Phe Ser Asp Arg Glu Ile Gln Phe
 180 185 190
 Val Leu Asp Pro Ala Ser Leu Ile Thr Ala Gln Asn Ile Val Leu Ser
 195 200 205
 Asn Leu Gln Ser Asn Gly Thr Gly Ala Cys Thr Ile Ser Gly Asn Thr
 210 215 220
 Gln Thr Gln Ile Phe Ser Asn Ser Val Asn Thr Thr Ala Asp Ser Gly
 225 230 235 240
 Gly Ala Phe Asp Met Val Thr Thr Ser Phe Thr Ala Ser Asp Asn Ala
 245 250 255
 Asn Leu Leu Phe Cys Asn Asn Tyr Cys Thr His Asn Lys Gly Gly Gly
 260 265 270
 Ala Ile Arg Ser Gly Gly Pro Ile Arg Phe Leu Asn Asn Gln Asp Val
 275 280 285
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 290 295 300
 Asp His Asn Glu Lys Asn Arg Gly Gly Ala Leu Tyr Ala Thr Thr Ile
 305 310 315 320
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 325 330 335
 Asp Cys Gly Gly Ala Ile Ser Ala Asp Thr Gln Ile Ser Ile Thr Asp
 340 345 350
 Thr Val Lys Gly Ile Leu Phe Glu Asn Asn His Thr Leu Asn His Ile
 355 360 365
 Pro Tyr Thr Gln Ala Glu Asn Met Ala Arg Gly Gly Ala Ile Cys Ser
 370 375 380
 Arg Arg Asp Leu Cys Ser Ile Ser Asn Asn Ser Gly Pro Ile Val Phe
 385 390 395 400
 Asn Tyr Asn Gln Gly Gly Lys Gly Gly Ala Ile Ser Ala Thr Arg Cys
 405 410 415
 Val Ile Asp Asn Asn Lys Glu Arg Ile Ile Phe Ser Asn Asn Ser Ser
 420 425 430
 Leu Gly Trp Ser Gln Ser Ser Ser Ala Ser Asn Gly Gly Ala Ile Gln
 435 440 445
 Thr Thr Gln Gly Phe Thr Leu Arg Asn Asn Lys Gly Ser Ile Tyr Phe
 450 455 460
 Asp Ser Asn Thr Ala Thr His Ala Gly Gly Ala Ile Asn Cys Gly Tyr
 465 470 475 480
 Ile Asp Ile Arg Asp Asn Gly Pro Val Tyr Phe Leu Asn Asn Ser Ala
 485 490 495
 Ala Trp Gly Ala Ala Phe Asn Leu Ser Lys Pro Arg Ser Ala Thr Asn
 500 505 510
 Tyr Ile His Thr Gly Thr Gly Asp Ile Val Phe Asn Asn Asn Val Val
 515 520 525
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 545 550 555 560
 Asp Thr Arg Ile Tyr Phe Tyr Asp Leu Phe Gln Trp Glu Arg Val Lys
 565 570 575
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 580 585 590
 Thr Val Asn Pro Glu Thr Glu Phe Ser Gly Ala Val Val Phe Ser Tyr
 595 600 605
 Asn Gln Met Ser Ser Asp Ile Arg Thr Leu Met Gly Lys Glu His Asn
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 625 630 635 640

Glu Asp Asp Ala Glu Leu
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<210> 318

<211> 34

<212> DNA

<213> *Chlamydia trachomatis*

<400> 318

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34

<210> 319

<211> 33

<212> DNA

<213> *Chlamydia trachomatis*

<400> 319

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33

<210> 320

<211> 2148

<212> DNA

<213> *Chlamydia trachomatis*

<400> 320

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<210> 321

<211> 715

<212> PRT

<213> Chlamydia trachomatis

<400> 321

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Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
35     40     45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
50     55     60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65     70     75
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
85     90     95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
100    105    110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
115    120    125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
130    135    140
Arg Pro Leu Asp Ile Arg Thr Leu Met Gly Lys Glu His Asn Tyr Ile
145    150    155
Lys Glu Ala Pro Thr Thr Leu Lys Phe Gly Thr Leu Ala Ile Glu Asp
165    170    175
Asp Ala Glu Leu Glu Ile Phe Asn Ile Pro Phe Thr Gln Asn Pro Thr
180    185    190
Ser Leu Leu Ala Leu Gly Ser Gly Ala Thr Leu Thr Val Gly Lys His
195    200    205
Gly Lys Leu Asn Ile Thr Asn Leu Gly Val Ile Leu Pro Ile Ile Leu
210    215    220
Lys Glu Gly Lys Ser Pro Pro Cys Ile Arg Val Asn Pro Gln Asp Met
225    230    235
Thr Gln Asn Thr Gly Thr Gly Gln Thr Pro Ser Ser Thr Ser Ser Ile
245    250    255
Ser Thr Pro Met Ile Ile Phe Asn Gly Arg Leu Ser Ile Val Asp Glu
260    265    270
Asn Tyr Glu Ser Val Tyr Asp Ser Met Asp Leu Ser Arg Gly Lys Ala
275    280    285
Glu Gln Leu Ile Leu Ser Ile Glu Thr Thr Asn Asp Gly Gln Leu Asp
290    295    300
Ser Asn Trp Gln Ser Ser Leu Asn Thr Ser Leu Leu Ser Pro Pro His
305    310    315
Tyr Gly Tyr Gln Gly Leu Trp Thr Pro Asn Trp Ile Thr Thr Thr Tyr
325    330    335
Thr Ile Thr Leu Asn Asn Asn Ser Ser Ala Pro Thr Ser Ala Thr Ser
340    345    350
Ile Ala Glu Gln Lys Lys Thr Ser Glu Thr Phe Thr Pro Ser Asn Thr
355    360    365
Thr Thr Ala Ser Ile Pro Asn Ile Lys Ala Ser Ala Gly Ser Gly Ser
370    375    380

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Gly Ser Ala Ser Asn Ser Gly Glu Val Thr Ile Thr Lys His Thr Leu
 385 390 395 400
 Val Val Asn Trp Ala Pro Val Gly Tyr Ile Val Asp Pro Ile Arg Arg
 405 410 415
 Gly Asp Leu Ile Ala Asn Ser Leu Val His Ser Gly Arg Asn Met Thr
 420 425 430
 Met Gly Leu Arg Ser Leu Leu Pro Asp Asn Ser Trp Phe Ala Leu Gln
 435 440 445
 Gly Ala Ala Thr Thr Leu Phe Thr Lys Gln Gln Lys Arg Leu Ser Tyr
 450 455 460
 His Gly Tyr Ser Ser Ala Ser Lys Gly Tyr Thr Val Ser Ser Gln Ala
 465 470 475 480
 Ser Gly Ala His Gly His Lys Phe Leu Leu Ser Phe Ser Gln Ser Ser
 485 490 495
 Asp Lys Met Lys Glu Lys Glu Thr Asn Asn Arg Leu Ser Ser Arg Tyr
 500 505 510
 Tyr Leu Ser Ala Leu Cys Phe Glu His Pro Met Phe Asp Arg Ile Ala
 515 520 525
 Leu Ile Gly Ala Ala Ala Cys Asn Tyr Gly Thr His Asn Met Arg Ser
 530 535 540
 Phe Tyr Gly Thr Lys Lys Ser Ser Lys Gly Lys Phe His Ser Thr Thr
 545 550 555 560
 Leu Gly Ala Ser Leu Arg Cys Glu Leu Arg Asp Ser Met Pro Leu Arg
 565 570 575
 Ser Ile Met Leu Thr Pro Phe Ala Gln Ala Leu Phe Ser Arg Thr Glu
 580 585 590
 Pro Ala Ser Ile Arg Glu Ser Gly Asp Leu Ala Arg Leu Phe Thr Leu
 595 600 605
 Glu Gln Ala His Thr Ala Val Val Ser Pro Ile Gly Ile Lys Gly Ala
 610 615 620
 Tyr Ser Ser Asp Thr Trp Pro Thr Leu Ser Trp Glu Met Glu Leu Ala
 625 630 635 640
 Tyr Gln Pro Thr Leu Tyr Trp Lys Arg Pro Leu Leu Asn Thr Leu Leu
 645 650 655
 Ile Gln Asn Asn Gly Ser Trp Val Thr Thr Asn Thr Pro Leu Ala Lys
 660 665 670
 His Ser Phe Tyr Gly Arg Gly Ser His Ser Leu Lys Phe Ser His Leu
 675 680 685
 Lys Leu Phe Ala Asn Tyr Gln Ala Glu Val Ala Thr Ser Thr Val Ser
 690 695 700
 His Tyr Ile Asn Ala Gly Gly Ala Leu Val Phe
 705 710 715

<210> 322

<211> 37

<212> DNA

<213> Chlamydia trachomatis

<400> 322

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37

<210> 323

<211> 36

<212> DNA

<213> Chlamydia trachomatis

<400> 323

gagagcgccc gcttacacag atccattacc ggactg

36

<210> 324
<211> 1896
<212> DNA
<213> Chlamydia trachomatis

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ccatcacact ggcggcgctg catgcctttt tctttgagat ctacatcatt ttgtttttta 480
gcttgtttgt gtctctatc gtatggattc gcgagctctc ctcaagtgtt aacacctaat 540
gtaaccactc cttttaaggg ggacgatgtt tacttgaatg gagaactgcg ttttgtcaat 600
gtctatgcag gggcagagaa cggctcaatt atctcagcta atggcgacaa tttaacgatt 660
accggacaaa accatacatt atcatttaca gattctcaag ggccagttct tcaaaattat 720
gccttcattt cagcaggaga gacacttact ctgaaagatt tttcgagttt gatgttctcg 780
aaaaattgtt ctctgcggaa aaagggaatg atctcagggg tatttccgga 840
gcaggcgaa gttatttttg ggataactct gtgggggtatt ctctttgtc tatttgtcca 900
gcatcgactc caactcctcc agcaccagca ccagctcctg ctgcttcaag ctctttatct 960
cacaacagtta gtgatgctcg gaaagggtct atttttctg tagagactag tttggagatc 1020
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<210> 325
<211> 631
<212> PRT
<213> Chlamydia trachomatis

<400> 325
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20 25 30
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35 40 45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
50 55 60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65 70 75 80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
85 90 95

Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
 100 105 110
 Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
 115 120 125
 Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
 130 135 140
 Arg Pro Leu Met Pro Phe Ser Leu Arg Ser Thr Ser Phe Cys Phe Leu
 145 150 155 160
 Ala Cys Leu Cys Ser Tyr Ser Tyr Gly Phe Ala Ser Ser Pro Gln Val
 165 170 175
 Leu Thr Pro Asn Val Thr Thr Pro Phe Lys Gly Asp Asp Val Tyr Leu
 180 185 190
 Asn Gly Asp Cys Ala Phe Val Asn Val Tyr Ala Gly Ala Glu Asn Gly
 195 200 205
 Ser Ile Ile Ser Ala Asn Gly Asp Asn Leu Thr Ile Thr Gly Gln Asn
 210 215 220
 His Thr Leu Ser Phe Thr Asp Ser Gln Gly Pro Val Leu Gln Asn Tyr
 225 230 235 240
 Ala Phe Ile Ser Ala Gly Glu Thr Leu Thr Leu Lys Asp Phe Ser Ser
 245 250 255
 Leu Met Phe Ser Lys Asn Val Ser Cys Gly Glu Lys Gly Met Ile Ser
 260 265 270
 Gly Lys Thr Val Ser Ile Ser Gly Ala Gly Glu Val Ile Phe Thr Asp
 275 280 285
 Asn Ser Val Gly Tyr Ser Pro Leu Ser Ile Val Pro Ala Ser Thr Pro
 290 295 300
 Thr Pro Pro Ala Pro Ala Pro Ala Ala Ser Ser Ser Leu Ser
 305 310 315 320
 Pro Thr Val Ser Asp Ala Arg Lys Gly Ser Ile Phe Ser Val Glu Thr
 325 330 335
 Ser Leu Glu Ile Ser Gly Val Lys Lys Gly Val Met Phe Asp Asn Asn
 340 345 350
 Ala Gly Asn Phe Gly Thr Val Phe Arg Gly Asn Ser Asn Asn Ala
 355 360 365
 Gly Ser Gly Gly Ser Gly Ser Ala Thr Thr Pro Ser Phe Thr Val Lys
 370 375 380
 Asn Cys Lys Gly Lys Val Ser Phe Thr Asp Asn Val Ala Ser Cys Gly
 385 390 395 400
 Gly Gly Val Val Tyr Lys Gly Thr Val Leu Phe Lys Asp Asn Glu Gly
 405 410 415
 Gly Ile Phe Phe Arg Gly Asn Thr Ala Tyr Asp Asp Leu Gly Ile Leu
 420 425 430
 Ala Ala Thr Ser Arg Asp Gln Asn Thr Glu Thr Gly Gly Gly Gly
 435 440 445
 Val Ile Cys Ser Pro Asp Asp Ser Val Lys Phe Glu Gly Asn Lys Gly
 450 455 460
 Ser Ile Val Phe Asp Tyr Asn Phe Ala Lys Gly Arg Gly Gly Ser Ile
 465 470 475 480
 Leu Thr Lys Glu Phe Ser Leu Val Ala Asp Asp Ser Val Val Phe Ser
 485 490 495
 Asn Asn Thr Ala Glu Lys Gly Gly Gly Ala Ile Tyr Ala Pro Thr Ile
 500 505 510
 Asp Ile Ser Thr Asn Gly Gly Ser Ile Leu Phe Glu Arg Asn Arg Ala
 515 520 525
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<211> 40
<212> DNA
<213> Chlamydia trachomatis
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<400> 326
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<210> 327
<211> 33
<212> DNA
<213> Chlamydia trachomatis
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<400> 327
gagagcggcc gcttaaaaga ttctattcaa gcc 33

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<210> 328
<211> 2148
<212> DNA
<213> Chlymadia trachomatis
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taatttaacg	aagatgatcg	gggtggcttt	ttagttagat	atggggggat	cacggcgacc	1380
cgacgctccc	aatatgaaaa	tggtccaata	tttggagttg	cttttgggac	acctctatgt	1440
gcacacaaag	gcacaaatga	ttactctaaa	gatctctgga	acatgaacat	qttctctctg	1500

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<210> 329

<211> 715

<212> PRT

<213> Chlamydia trachomatis

<400> 329

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Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
35 40 45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
50 55 60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65 70 75 80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
85 90 95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
100 105 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
115 120 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
130 135 140
Arg Pro Leu Asp Pro Val Val Gln Asn Asn Ser Ala Ala Gly Ala Ser
145 150 155 160
Thr Pro Ser Pro Ser Ser Ser Ser Met Pro Gly Ala Val Thr Ile Asn
165 170 175
Gln Ser Gly Asn Gly Ser Val Ile Phe Thr Ala Glu Ser Leu Thr Pro
180 185 190
Ser Glu Lys Leu Gln Val Leu Asn Ser Thr Ser Asn Phe Pro Gly Ala
195 200 205
Leu Thr Val Ser Gly Gly Glu Leu Val Val Thr Glu Gly Ala Thr Leu
210 215 220
Thr Thr Gly Thr Ile Thr Ala Thr Ser Gly Arg Val Thr Leu Gly Ser
225 230 235 240
Gly Ala Ser Leu Ser Ala Val Ala Gly Ala Ala Asn Asn Asn Tyr Thr
245 250 255
Cys Thr Val Ser Lys Leu Gly Ile Asp Leu Glu Ser Phe Leu Thr Pro
260 265 270
Asn Tyr Lys Thr Ala Ile Leu Gly Ala Asp Gly Thr Val Thr Val Asn
275 280 285
Ser Gly Ser Thr Leu Asp Leu Val Met Glu Asn Glu Ala Glu Val Tyr
290 295 300
Asp Asn Pro Leu Phe Val Gly Ser Leu Thr Ile Pro Phe Val Thr Leu
305 310 315 320

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Ser	Ser	Ser	Ser	Ala	Ser	Asn	Gly	Val	Thr	Lys	Asn	Ser	Val	Thr	Ile
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Asn	Asp	Ala	Asp	Ala	Ala	His	Tyr	Gly	Tyr	Gln	Gly	Ser	Trp	Ser	Ala
340				340				345					350		
Asp	Trp	Thr	Lys	Pro	Pro	Leu	Ala	Pro	Asp	Ala	Lys	Gly	Met	Val	Pro
355							360					365			
Pro	Asn	Thr	Asn	Asn	Thr	Leu	Tyr	Leu	Thr	Trp	Arg	Pro	Ala	Ser	Asn
370							375								
Tyr	Gly	Glu	Tyr	Arg	Leu	Asp	Pro	Gln	Arg	Lys	Gly	Glu	Leu	Val	Pro
385					390					395					400
Asn	Ser	Leu	Trp	Val	Ala	Gly	Ser	Ala	Leu	Arg	Thr	Phe	Thr	Asn	Gly
405								410						415	
Leu	Lys	Glu	His	Tyr	Val	Ser	Arg	Asp	Val	Gly	Phe	Val	Ala	Ser	Leu
420								425					430		
His	Ala	Leu	Gly	Asp	Tyr	Ile	Leu	Asn	Tyr	Thr	Gln	Asp	Asp	Arg	Asp
435							440					445			
Gly	Phe	Leu	Ala	Arg	Tyr	Gly	Gly	Phe	Gln	Ala	Thr	Ala	Ala	Ser	His
450						455					460				
Tyr	Glu	Asn	Gly	Ser	Ile	Phe	Gly	Val	Ala	Phe	Gly	Gln	Leu	Tyr	Gly
465					470					475					480
Gln	Thr	Lys	Ser	Arg	Met	Tyr	Tyr	Ser	Lys	Asp	Ala	Gly	Asn	Met	Thr
485								490						495	
Met	Leu	Ser	Cys	Phe	Gly	Arg	Ser	Tyr	Val	Asp	Ile	Lys	Gly	Thr	Glu
500								505					510		
Thr	Val	Met	Tyr	Trp	Glu	Thr	Ala	Tyr	Gly	Tyr	Ser	Val	His	Arg	Met
515							520					525			
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530						535					540				
Cys	His	Trp	His	Asn	Asn	Asn	Tyr	Tyr	Ala	Phe	Val	Gly	Ala	Glu	His
545				550						555					560
Asn	Phe	Leu	Glu	Tyr	Cys	Ile	Pro	Thr	Arg	Gln	Leu	Ala	Arg	Asp	Tyr
565								570						575	
Glu	Leu	Thr	Gly	Phe	Met	Arg	Phe	Glu	Met	Ala	Gly	Gly	Trp	Ser	Ser
580								585					590		
Ser	Thr	Arg	Glu	Thr	Gly	Ser	Leu	Thr	Arg	Tyr	Phe	Ala	Arg	Gly	Ser
595							600					605			
Gly	His	Asn	Met	Ser	Leu	Pro	Ile	Gly	Ile	Val	Ala	His	Ala	Val	Ser
610						615					620				
His	Val	Arg	Arg	Ser	Pro	Pro	Ser	Lys	Leu	Thr	Leu	Asn	Met	Gly	Tyr
625					630					635					640
Arg	Pro	Asp	Ile	Trp	Arg	Val	Thr	Pro	His	Cys	Asn	Met	Glu	Ile	Ile
645								650						655	
Ala	Asn	Gly	Val	Lys	Thr	Pro	Ile	Gln	Gly	Ser	Pro	Leu	Ala	Arg	His
660								665					670		
Ala	Phe	Phe</													

<210> 330

<211> 38

<212> DNA

<213> Chlamydia trachomatis

<400> 330

gagagcggcc gctcatgaaa tggctgtcag ctactgcc

<210> 331
 <211> 34
 <212> DNA
 <213> Chlymadia trachomatis

<400> 331
 gagcgccgc ttacttaagt cgaatttctt caag

34

<210> 332
 <211> 1557
 <212> DNA
 <213> Chlymadia trachomatis

<400> 332
 atgcatacc atcaccatca cagggccgcg tccgataact tccagctgtc ccagggtggg 60
 cagggaattc ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120
 accgttcata tcgggcctac cgccttcttc ggcttgggtg ttgtcgacaa caacggcaac 180
 ggcgacagag tcacacgcgt ggtcgggagc gctcggcgcg caagtctcgg catctccacc 240
 ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggag 300
 gcgcttaacg ggcatacctc cgggtgacgtc atctcggtga cctggcacaac caagtcgggc 360
 ggacgcgcta cagggaacgt gacattggcc gagggaccgc cggccgaatt ctgcagatat 420
 ccatcacact ggccggccgct catgaaatgg ctgtcagcta ctgcggtgtt tgctcgtgtt 480
 ctccctcaag ttctcagggtt ttgcttccca gaacctaaag aattaaattt ctctcgcgta 540
 gaaacttctt cctctaccac ttttactgaa acaattggag aagctggggc agaataatc 600
 gtctctggta agcgtatctt cacaataatt accaacattc ctactaccga tacaacaact 660
 cccaggaact caaactcctc tagctctagc ggagaaactg cttccgtttc tgaggtagtg 720
 gactctacaa caacgactcc tgatctaaag ggtggcgcg ccttttataa cgcgcactcc 780
 ggagtttgtt cctttatgac acgatcagga acagaaggtt ccttaactct gttcgagata 840
 aaaatgactg gtgaaggcg tgctatcttc tctcaaggag agctgctatt tacagatctg 900
 acaagtctaa ccatccaaaa taacttatcc cagctatccg gagggagcgt ttctggagga 960
 tctacaactc ccctatcagg gattactaaa cgcactttct cctgcaactc tgcagaagtt 1020
 cctgctcctg ttaagaagac tacagaacct aaagctcaaa cagcaagcga aacgtcgggt 1080
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 attcaatctt ctaaaacag ctctttttaa tctaactaca gtaaaccaag tgggggggct 1500
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<210> 333
 <211> 518
 <212> PRT
 <213> Chlymadia trachomatis

<400> 333
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 20 25 30
 Ile Ala Gly Gly Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
 35 40 45
 Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
 50 55 60
 Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
 65 70 75 80

Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
 85 90 95
 Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
 100 105 110
 Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
 115 120 125
 Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
 130 135 140
 Arg Pro Leu Met Lys Trp Leu Ser Ala Thr Ala Val Phe Ala Ala Val
 145 150 155 160
 Leu Pro Ser Val Ser Gly Phe Cys Phe Pro Glu Pro Lys Glu Leu Asn
 165 170 175
 Phe Ser Arg Val Glu Thr Ser Ser Ser Thr Thr Phe Thr Glu Thr Ile
 180 185 190
 Gly Glu Ala Gly Ala Glu Tyr Ile Val Ser Gly Asn Ala Ser Phe Thr
 195 200 205
 Lys Phe Thr Asn Ile Pro Thr Thr Asp Thr Thr Thr Pro Thr Asn Ser
 210 215 220
 Asn Ser Ser Ser Ser Ser Gly Glu Thr Ala Ser Val Ser Glu Asp Ser
 225 230 235 240
 Asp Ser Thr Thr Thr Thr Pro Asp Pro Lys Gly Gly Ala Phe Tyr
 245 250 255
 Asn Ala His Ser Gly Val Leu Ser Phe Met Thr Arg Ser Gly Thr Glu
 260 265 270
 Gly Ser Leu Thr Leu Ser Glu Ile Lys Met Thr Gly Glu Gly Gly Ala
 275 280 285
 Ile Phe Ser Gln Gly Glu Leu Leu Phe Thr Asp Leu Thr Ser Leu Thr
 290 295 300
 Ile Gln Asn Asn Leu Ser Gln Leu Ser Gly Gly Ala Ile Phe Gly Gly
 305 310 315 320
 Ser Thr Ile Ser Leu Ser Gly Ile Thr Lys Ala Thr Phe Ser Cys Asn
 325 330 335
 Ser Ala Glu Val Pro Ala Pro Val Lys Lys Pro Thr Glu Pro Lys Ala
 340 345 350
 Gln Thr Ala Ser Glu Thr Ser Gly Ser Ser Ser Ser Ser Gly Asn Asp
 355 360 365
 Ser Val Ser Ser Pro Ser Ser Ser Arg Ala Glu Pro Ala Ala Ala Asn
 370 375 380
 Leu Gln Ser His Phe Ile Cys Ala Thr Ala Thr Pro Ala Ala Gln Thr
 385 390 395 400
 Asp Thr Glu Thr Ser Thr Pro Ser His Lys Pro Gly Ser Gly Gly Ala
 405 410 415
 Ile Tyr Ala Lys Gly Asp Leu Thr Ile Ala Asp Ser Gln Glu Val Leu
 420 425 430
 Phe Ser Ile Asn Lys Ala Thr Lys Asp Gly Gly Ala Ile Phe Ala Glu
 435 440 445
 Lys Asp Val Ser Phe Glu Asn Ile Thr Ser Leu Lys Val Gln Thr Asn
 450 455 460
 Gly Ala Glu Glu Lys Gly Gly Ala Ile Tyr Ala Lys Gly Asp Leu Ser
 465 470 475 480
 Ile Gln Ser Ser Lys Gln Ser Leu Phe Asn Ser Asn Tyr Ser Lys Gln
 485 490 495
 Gly Gly Gly Ala Leu Tyr Val Glu Gly Gly Ile Asn Phe Gln Asp Leu
 500 505 510
 Glu Glu Ile Arg Ile Lys
 515

<211> 37
 <212> DNA
 <213> Chlamydia trachomatis

 <400> 334
 gagagcggcc gctcgggtgac ctctcaattc aatcttcc 37

 <210> 335
 <211> 39
 <212> DNA
 <213> Chlamydia trachomatis

 <400> 335
 gagagcggcc gcttagttct ctgttacaga taaggagac 39

 <210> 336
 <211> 1758
 <212> DNA
 <213> Chlamydia trachomatis

 <400> 336
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 accgttcata tggggcctac cgccttcttc ggcttgggtg ttgtcgacaa caacgggcaac 180
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 ggccttaacg ggcacatccc cgggtgacgtc atctcgggtga cctggcacaac caagtccggc 360
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 ccattcacct ggccgcgct cgggtgacct tcaattcaat ctcttaacaa gactcttttt 480
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 gagataggtg gaggtatctg ctgtaagaa tctttagaac tagatgctct agtctctcta 1740
 tctgtaacag agaactaa 1758

 <210> 337
 <211> 585
 <212> PRT
 <213> Chlamydia trachomatis

 <400> 337

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 20 25 30
 Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
 35 40 45
 Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
 50 55 60
 Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
 65 70 75 80
 Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
 85 90 95
 Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
 100 105 110
 Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
 115 120 125
 Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
 130 135 140
 Arg Pro Leu Gly Asp Leu Ser Ile Gln Ser Ser Lys Gln Ser Leu Phe
 145 150 155 160
 Asn Ser Asn Tyr Ser Lys Gln Gly Gly Gly Ala Leu Tyr Val Glu Gly
 165 170 175
 Gly Ile Asn Phe Gln Asp Leu Glu Glu Ile Arg Ile Lys Tyr Asn Lys
 180 185 190
 Ala Gly Thr Phe Glu Thr Lys Lys Ile Thr Leu Pro Ser Leu Lys Ala
 195 200 205
 Gln Ala Ser Ala Gly Asn Ala Asp Ala Trp Ala Ser Ser Pro Gln
 210 215 220
 Ser Gly Ser Gly Ala Thr Thr Val Ser Asp Ser Gly Asp Ser Ser Ser
 225 230 235 240
 Gly Ser Asp Ser Asp Thr Ser Glu Thr Val Pro Val Thr Ala Lys Gly
 245 250 255
 Gly Gly Leu Tyr Thr Asp Lys Asn Leu Ser Ile Thr Asn Ile Thr Gly
 260 265 270
 Ile Ile Glu Ile Ala Asn Asn Lys Ala Thr Asp Val Gly Gly Ala
 275 280 285
 Tyr Val Lys Gly Thr Leu Thr Cys Glu Asn Ser His Arg Leu Gln Phe
 290 295 300
 Leu Lys Asn Ser Ser Asp Lys Gln Gly Gly Gly Ile Tyr Gly Glu Asp
 305 310 315 320
 Asn Ile Thr Leu Ser Asn Leu Thr Gly Lys Thr Leu Phe Gln Glu Asn
 325 330 335
 Thr Ala Lys Glu Glu Gly Gly Gly Leu Phe Ile Lys Gly Thr Asp Lys
 340 345 350
 Ala Leu Thr Met Thr Gly Leu Asp Ser Phe Cys Leu Ile Asn Asn Thr
 355 360 365
 Ser Glu Lys His Gly Gly Ala Phe Val Thr Lys Glu Ile Ser Gln
 370 375 380
 Thr Tyr Thr Ser Asp Val Glu Thr Ile Pro Gly Ile Thr Pro Val His
 385 390 395 400
 Gly Glu Thr Val Ile Thr Gly Asn Lys Ser Thr Gly Gly Asn Gly Gly
 405 410 415
 Gly Val Cys Thr Lys Arg Leu Ala Leu Ser Asn Leu Gln Ser Ile Ser
 420 425 430
 Ile Ser Gly Asn Ser Ala Ala Glu Asn Gly Gly Ala His Thr Cys
 435 440 445
 Pro Asp Ser Phe Pro Thr Ala Asp Thr Ala Glu Gln Pro Ala Ala Ala
 450 455 460

Ser Ala Ala Thr Ser Thr Pro Lys Ser Ala Pro Val Ser Thr Ala Leu
 465 470 475 480
 Ser Thr Pro Ser Ser Ser Thr Val Ser Ser Leu Thr Leu Ala Ala
 485 490 495
 Ser Ser Gln Ala Ser Pro Ala Thr Ser Asn Lys Glu Thr Gln Asp Pro
 500 505 510
 Asn Ala Asp Thr Asp Leu Leu Ile Asp Tyr Val Val Asp Thr Thr Ile
 515 520 525
 Ser Lys Asn Thr Ala Lys Lys Gly Gly Gly Ile Tyr Ala Lys Lys Ala
 530 535 540
 Lys Met Ser Arg Ile Asp Gln Leu Asn Ile Ser Glu Asn Ser Ala Thr
 545 550 555 560
 Glu Ile Gly Gly Gly Ile Cys Cys Lys Glu Ser Leu Glu Leu Asp Ala
 565 570 575
 Leu Val Ser Leu Ser Val Thr Glu Asn
 580 585

<210> 338

<211> 38

<212> DNA

<213> Chlamydia trachomatis

<400> 338

gagagcggcc gctcgaccaa ctgaatatct ctgagaac

38

<210> 339

<211> 35

<212> DNA

<213> Chlamydia trachomatis

<400> 339

gagagcggcc gcttaagaga ctacgtggag ttctg

35

<210> 340

<211> 1965

<212> DNA

<213> Chlamydia trachomatis

<400> 340

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accgttcata	tccggccctac	cgcttctctc	ggcttgggtg	ttgtcgacaa	caacggccaac	180
ggcgacagag	tccaacgcgt	ggtcggggagc	gctccggcgg	caagtctcgg	catctccacc	240
ggcgacgtga	tcacccgcgt	cgacggcgct	ccgatcaact	cgccacccgc	gatggcggac	300
ggccttaacg	ggcatcatcc	cggtgacgtc	atctcgggtg	cctggcacaac	caagtcgggc	360
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ccatcacact	ggcgccgcgt	cgaccaactg	aatatctctg	agaactccgc	tacagagata	480
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aatctgaaat	caggctctct	ttctcgaaac	aacaaagcaa	actctctcat	cacaggagtc	660
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gataacaatc	cctcccaatc	atcgttgaac	gtacaaggag	gagccatcta	tgccaaaacc	900
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tccactggga	aatctcaaac	aacaggggca	atagcgggag	gagcgatata	ctccctctat	1020
gttacatgga	attgtctctg	gacattctct	aacaatacag	cctctatagc	tacaccgaag	1080
actttctctg	aagatggatc	ctcaggaaat	tctattaaag	ataccattgg	aggagccatt	1140

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gcagggacag ccattaccct atctggagtc tctcgatttt cagggaaatc ggctgattta 1200
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tctctggaat tacatgaaaa caaatcttac atcccacaga atgcaatctc tcacaacgga 1920
actttagttc ttaaagagaa aacagaactc cactagttct ctttaa 1965

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<210> 341

<211> 654

<212> PRT

<213> Chlamydia trachomatis

<400> 341

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Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
35 40 45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
50 55 60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65 70 75 80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
85 90 95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
100 105 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
115 120 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
130 135 140
Arg Pro Leu Asp Gln Leu Asn Ile Ser Glu Asn Ser Ala Thr Glu Ile
145 150 155 160
Gly Gly Gly Ile Cys Cys Lys Glu Ser Leu Glu Leu Asp Ala Leu Val
165 170 175
Ser Leu Ser Val Thr Glu Asn Leu Val Gly Lys Glu Gly Gly Gly Leu
180 185 190
His Ala Lys Thr Val Asn Ile Ser Asn Leu Lys Ser Gly Phe Ser Phe
195 200 205
Ser Asn Asn Lys Ala Asn Ser Ser Ser Thr Gly Val Ala Thr Thr Ala
210 215 220
Ser Ala Pro Ala Ala Ala Ala Ala Ser Leu Gln Ala Ala Ala Ala Ala
225 230 235 240
Ala Pro Ser Ser Pro Ala Thr Pro Thr Tyr Ser Gly Val Val Gly Gly
245 250 255
Ala Ile Tyr Gly Glu Lys Val Thr Phe Ser Gln Cys Ser Gly Thr Cys
260 265 270
Gln Phe Ser Gly Asn Gln Ala Ile Asp Asn Asn Pro Ser Gln Ser Ser
275 280 285
Leu Asn Val Gln Gly Gly Ala Ile Tyr Ala Lys Thr Ser Leu Ser Ile

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Gly Ser Ser Asp Ala Gly Thr Ser Tyr Ile Phe Ser Gly Asn Ser Val
305              310              315              320
Ser Thr Gly Lys Ser Gln Thr Thr Gly Gln Ile Ala Gly Gly Ala Ile
      325              330              335
Tyr Ser Pro Thr Val Thr Leu Asn Cys Pro Ala Thr Phe Ser Asn Asn
      340              345              350
Thr Ala Ser Ile Ala Thr Pro Lys Thr Ser Ser Glu Asp Gly Ser Ser
      355              360              365
Gly Asn Ser Ile Lys Asp Thr Ile Gly Gly Ala Ile Ala Gly Thr Ala
      370              375              380
Ile Thr Leu Ser Gly Val Ser Arg Phe Ser Gly Asn Thr Ala Asp Leu
385              390              395              400
Gly Ala Ala Ile Gly Thr Leu Ala Asn Ala Asn Thr Pro Ser Ala Thr
      405              410              415
Ser Gly Ser Gln Asn Ser Ile Thr Glu Lys Ile Thr Leu Glu Asn Gly
      420              425              430
Ser Phe Ile Phe Glu Arg Asn Gln Ala Asn Lys Arg Gly Ala Ile Tyr
      435              440              445
Ser Pro Ser Val Ser Ile Lys Gly Asn Asn Ile Thr Phe Asn Gln Asn
      450              455              460
Thr Ser Thr His Asp Gly Ser Ala Ile Tyr Phe Thr Lys Asp Ala Thr
465              470              475              480
Ile Glu Ser Leu Gly Ser Val Leu Phe Thr Gly Asn Asn Val Thr Ala
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Thr Gln Ala Ser Ser Ala Thr Ser Gly Gln Asn Thr Asn Thr Ala Asn
      500              505              510
Tyr Gly Ala Ala Ile Phe Gly Asp Pro Gly Thr Thr Gln Ser Ser Gln
      515              520              525
Thr Asp Ala Ile Leu Thr Leu Leu Ala Ser Ser Gly Asn Ile Thr Phe
      530              535              540
Ser Asn Asn Ser Leu Gln Asn Asn Gln Gly Asp Thr Pro Ala Ser Lys
545              550              555              560
Phe Cys Ser Ile Ala Gly Tyr Val Lys Leu Ser Leu Gln Ala Ala Lys
      565              570              575
Gly Lys Thr Ile Ser Phe Phe Asp Cys Val His Thr Ser Thr Lys Lys
      580              585              590
Thr Gly Ser Thr Gln Asn Val Tyr Glu Thr Leu Asp Ile Asn Lys Glu
      595              600              605
Glu Asn Ser Asn Pro Tyr Thr Gly Thr Ile Val Phe Ser Ser Glu Leu
610              615              620
His Glu Asn Lys Ser Tyr Ile Pro Gln Asn Ala Ile Leu His Asn Gly
625              630              635              640
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<210> 342

<211> 36

<212> DNA

<213> Chlamydia trachomatis

<400> 342

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36

<210> 343

<211> 35

<212> DNA

<213> Chlamydia trachomatis

<400> 343
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35

<210> 344
<211> 2103
<212> DNA
<213> Chlamydia trachomatis

<400> 344
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ttgtcttcca atgaaagtgc tcaagtcttc tgcggagtgc caactagacac cctctgtaga 1980
gcagaataca gtactcaact atactctggt cctctctgga cctctcaggg aaactatact 2040
atcgatgtag gcatgtatc gctatcgcaa atgactagct gcgggtgctg catgatcttc 2100
taa 2103

<210> 345
<211> 700
<212> PRT
<213> Chlamydia trachomatis

<400> 345
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1 5 10 15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
20 25 30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala

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      35              40              45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
  50              55              60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
  65              70              75              80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
      85              90              95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
      100              105              110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
      115              120              125
Leu Ala Gly Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
      130              135              140
Arg Pro Leu Gly Thr Ile Val Phe Ser Ser Glu Leu His Glu Asn Lys
      145              150              155              160
Ser Tyr Ile Pro Gln Asn Ala Ile Leu His Asn Gly Thr Leu Val Leu
      165              170              175
Lys Glu Lys Thr Glu Leu His Val Val Ser Phe Glu Gln Lys Glu Gly
      180              185              190
Ser Lys Leu Ile Met Glu Pro Gly Ala Val Leu Ser Asn Gln Asn Ile
      195              200              205
Ala Asn Gly Ala Leu Ala Ile Asn Gly Leu Thr Ile Asp Leu Ser Ser
      210              215              220
Met Gly Thr Pro Gln Ala Gly Glu Ile Phe Ser Pro Pro Glu Leu Arg
      225              230              235              240
Ile Val Ala Thr Thr Ser Ser Ala Ser Gly Gly Ser Gly Val Ser Ser
      245              250              255
Ser Ile Pro Thr Asn Pro Lys Arg Ile Ser Ala Ala Val Pro Ser Gly
      260              265              270
Ser Ala Ala Thr Thr Pro Thr Met Ser Glu Asn Lys Val Phe Leu Thr
      275              280              285
Gly Asp Leu Thr Leu Ile Asp Pro Asn Gly Asn Phe Tyr Gln Asn Pro
      290              295              300
Met Leu Gly Ser Asp Leu Asp Val Pro Leu Ile Lys Leu Pro Thr Asn
      305              310              315              320
Thr Ser Asp Val Gln Val Tyr Asp Leu Thr Leu Ser Gly Asp Leu Phe
      325              330              335
Pro Gln Lys Gly Tyr Met Gly Thr Trp Thr Leu Asp Ser Asn Pro Gln
      340              345              350
Thr Gly Lys Leu Gln Ala Arg Trp Thr Phe Asp Thr Tyr Arg Arg Trp
      355              360              365
Val Tyr Ile Pro Arg Asp Asn His Phe Tyr Ala Asn Ser Ile Leu Gly
      370              375              380
Ser Gln Asn Ser Met Ile Val Val Lys Gln Gly Leu Ile Asn Asn Met
      385              390              395              400
Leu Asn Asn Ala Arg Phe Asp Asp Ile Ala Tyr Asn Asn Phe Trp Val
      405              410              415
Ser Gly Val Gly Thr Phe Leu Ala Gln Gln Gly Thr Pro Leu Ser Glu
      420              425              430
Glu Phe Ser Tyr Tyr Ser Arg Gly Thr Ser Val Ala Ile Asp Ala Lys
      435              440              445
Pro Arg Gln Asp Phe Ile Leu Gly Ala Ala Phe Ser Lys Ile Val Gly
      450              455              460
Lys Thr Lys Ala Ile Lys Lys Met His Asn Tyr Phe His Lys Gly Ser
      465              470              475              480
Glu Tyr Ser Tyr Gln Ala Ser Val Tyr Gly Gly Lys Phe Leu Tyr Phe
      485              490              495
Leu Leu Asn Lys Gln His Gly Trp Ala Leu Pro Phe Leu Ile Gln Gly

```

500	505	510
Val Val Ser Tyr Gly His Ile Lys His Asp Thr Thr Leu Tyr Pro		
515	520	525
Ser Ile His Glu Arg Asn Lys Gly Asp Trp Glu Asp Leu Gly Trp Leu		
530	535	540
Ala Asp Leu Arg Ile Ser Met Asp Leu Lys Glu Pro Ser Lys Asp Ser		
545	550	555
Ser Lys Arg Ile Thr Val Tyr Gly Glu Leu Glu Tyr Ser Ser Ile Arg		
565	570	575
Gln Lys Gln Phe Thr Glu Ile Asp Tyr Asp Pro Arg His Phe Asp Asp		
580	585	590
Cys Ala Tyr Arg Asn Leu Ser Leu Pro Val Gly Cys Ala Val Glu Gly		
595	600	605
Ala Ile Met Asn Cys Asn Ile Leu Met Tyr Asn Lys Leu Ala Leu Ala		
610	615	620
Tyr Met Pro Ser Ile Tyr Arg Asn Asn Pro Val Cys Lys Tyr Arg Val		
625	630	635
Leu Ser Ser Asn Glu Ala Gly Gln Val Ile Cys Gly Val Pro Thr Arg		
645	650	655
Thr Ser Ala Arg Ala Glu Tyr Ser Thr Gln Leu Tyr Leu Gly Pro Phe		
660	665	670
Trp Thr Leu Tyr Gly Asn Tyr Thr Ile Asp Val Gly Met Tyr Thr Leu		
675	680	685
Ser Gln Met Thr Ser Cys Gly Ala Arg Met Ile Phe		
690	695	700

<210> 346

<211> 37

<212> DNA

<213> Chlamydia trachomatis

<400> 346

gagagcgccc gctcatgaaa tttatgtcag ctactgc

37

<210> 347

<211> 37

<212> DNA

<213> Chlamydia trachomatis

<400> 347

gagagcgccc gcttaccctg taattccagt gatggtc

37

<210> 348

<211> 1464

<212> DNA

<213> Chlamydia trachomatis

<400> 348

atgcataacc	atcaccatca	cacggccgcg	tccgataact	tccagctgtc	ccagggtggg	60
cagggtattcg	ccattccgat	cgggcaggcg	atggcgatcg	cgggccagat	caagcttccc	120
accgttcata	tccggcctac	cgcttccctc	ggcttgggtg	ttgtcgacaa	caacggcaca	180
ggcgacagag	tccaaacgct	ggtcggggagc	gctccggcgg	caagtctcgg	catctccacc	240
ggcgacgtga	tcaccgcggt	cgacggcgct	ccgatcaact	cgggccaccgc	gatggcggac	300
gcgcttaacg	ggcatcatcc	cggtgacgtc	atctcgggtga	cctggcacaac	caagtcgggc	360
ggcagcgcta	cagggaacgt	gacattggcc	gagggacccc	cgggcgaatt	ctgcagatat	420
ccatcacact	ggcggcgctc	catgaaattt	atgtcagcta	ctgctgtatt	tgtgcagta	480
ctctctccg	ttactgagc	gagctcgatc	caagatcaaa	taaagaatac	cgactgcaat	540
gttagcaaa	taggatattc	aactttctca	gcatttactg	atatgatgct	agcagacaac	600

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acagagtatc gagctgctga tagtgtttca ttctatgact ttctgacatc ttccggatta 660
cctagaaaac atcttagtag tagtagtgaa gcttctccaa cgacagaagg agtgctttca 720
tcttcatctg gagaaaatac tgagaattca caagattcag ctccctcttc tggagaaact 780
gataagaaaa cagaagaaga actagacaat ggccgaatca tttatgctag agagaaaacta 840
actatctcag aatctcagga ctctctctct aatccaagca tagaactcca tgacaactagt 900
ttttttcttg gagaagggtga agttatcttt gatcacagag ttgcccctcaa aaacgggagga 960
gctatttatg gagagaaaaga ggtagtcttt gaaaacataa aatctctact agtagaagta 1020
aatatctcgg tcgagaaaagg gggtagcgctc tatgcaaaag aacgagtatc tttagaaaaat 1080
gttacccgaag caacctctct ctccaatggt ggggaacaaag gtggtggtgg aatctattca 1140
gaacaagata tgttaatcag tgattgcaac aatgtacatt tccaagggaa tgctcgagga 1200
gcaacagcag taaaacaatg tctggatgaa gaaatgatcg tattgtctac agaatgcggt 1260
gatagcttat ccgaagatac actggatagc actccagaaa ccgaacagac taagtcaaat 1320
ggaaatcaag atggttctgc tgaacacaaa gatacacaaag tatcagaatc accagaatca 1380
actctagccc ccgacgatgt tttaggtaaa ggtggtggtg tctatacaga aaaatctttg 1440
accatcactg gaattacagg gtaa 1464

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<210> 349

<211> 487

<212> FRT

<213> Chlamydia trachomatis

<400> 349

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Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1 5 10 15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
20 25 30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
35 40 45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
50 55 60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65 70 75 80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
85 90 95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
100 105 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
115 120 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
130 135 140
Arg Pro Leu Met Lys Phe Met Ser Ala Thr Ala Val Phe Ala Ala Val
145 150 155 160
Leu Ser Ser Val Thr Glu Ala Ser Ser Ile Gln Asp Gln Ile Lys Asn
165 170 175
Thr Asp Cys Asn Val Ser Lys Val Gly Tyr Ser Thr Ser Gln Ala Phe
180 185 190
Thr Asp Met Met Leu Ala Asp Asn Thr Glu Tyr Arg Ala Ala Asp Ser
195 200 205
Val Ser Phe Tyr Asp Phe Ser Thr Ser Ser Gly Leu Pro Arg Lys His
210 215 220
Leu Ser Ser Ser Ser Glu Ala Ser Pro Thr Thr Glu Gly Val Ser Ser
225 230 235 240
Ser Ser Ser Gly Glu Asn Thr Glu Asn Ser Gln Asp Ser Ala Pro Ser
245 250 255
Ser Gly Glu Thr Asp Lys Lys Thr Glu Glu Glu Leu Asp Asn Gly Gly
260 265 270
Ile Ile Tyr Ala Arg Glu Lys Leu Thr Ile Ser Glu Ser Gln Asp Ser
275 280 285

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Leu Ser Asn Pro Ser Ile Glu Leu His Asp Asn Ser Phe Phe Phe Gly
 290 295 300
 Glu Gly Glu Val Ile Phe Asp His Arg Val Ala Leu Lys Asn Gly Gly
 305 310 315 320
 Ala Ile Tyr Gly Glu Lys Glu Val Val Phe Glu Asn Ile Lys Ser Leu
 325 330 335
 Leu Val Glu Val Asn Ile Ser Val Glu Lys Gly Gly Ser Val Tyr Ala
 340 345 350
 Lys Glu Arg Val Ser Leu Glu Asn Val Thr Glu Ala Thr Phe Ser Ser
 355 360 365
 Asn Gly Gly Glu Gln Gly Gly Gly Ile Tyr Ser Glu Gln Asp Met
 370 375 380
 Leu Ile Ser Asp Cys Asn Asn Val His Phe Gln Gly Asn Ala Ala Gly
 385 390 395 400
 Ala Thr Ala Val Lys Gln Cys Leu Asp Glu Glu Met Ile Val Leu Leu
 405 410 415
 Thr Glu Cys Val Asp Ser Leu Ser Glu Asp Thr Leu Asp Ser Thr Pro
 420 425 430
 Glu Thr Glu Gln Thr Lys Ser Asn Gly Asn Gln Asp Gly Ser Ser Glu
 435 440 445
 Thr Lys Asp Thr Gln Val Ser Glu Ser Pro Glu Ser Thr Pro Ser Pro
 450 455 460
 Asp Asp Val Leu Gly Lys Gly Gly Ile Tyr Thr Glu Lys Ser Leu
 465 470 475 480
 Thr Ile Thr Gly Ile Thr Gly
 485

<210> 350

<211> 37

<212> DNA

<213> Chlamydia trachomatis

<400> 350

gagagcggcc gctcgatata caagtatcag aatcac

37

<210> 351

<211> 37

<212> DNA

<213> Chlamydia trachomatis

<400> 351

gagagcggcc gcttaagagg acgatgagac actctcg

37

<210> 352

<211> 1752

<212> DNA

<213> Chlamydia trachomatis

<400> 352

atgcatacc	atcaccatca	cacggccgcg	tccgataact	tcagctgtc	ccagggtggg	60
cagggtatcg	ccattccgat	cgggcaggcg	atggcgatcg	cgggccagat	caagcttccc	120
accgttcata	tcgggcctac	cgccttcctc	ggcttgggtg	ttgtcgacaa	caacggcaac	180
ggcgacagag	tcacaacgct	ggtcggggagc	gctcggcgcg	caagtctcgg	catctccacc	240
ggcgacgtga	tcaccgcggt	cgacggcgct	ccgatcaact	cggccaccgc	gatgcgggac	300
gcgcttaacg	ggcatcatcc	cggtgacgtc	atctcggtga	cctggcgaac	caagtcgggc	360
ggcacgcgta	cagggaacgt	gacattggcc	gagggaaccc	cggccgaatt	ctcgagatat	420
ccatcacact	ggcgccgcgt	cgatacacia	gtatcagaat	caccagaatc	aactcctagc	480
cccgcagatg	ttttaggtaa	aggtgggtggt	atctatacag	aaaaatcttt	gaccatcatc	540


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ggaattacag ggactataga tttgtcagt aacatagcta cagattctcg agcagggtga 600
ttcactaaag aaaactgtgc ttgcaccaac acgaatagcc tacagttttt gaaaactctg 660
gcagggtcaac atggaggagg agcctacgtt actcaaacca tgtctgttac taatacaact 720
agtgaagatga taactactcc cccctctogta ggagaagtga tttctcttga aatacacagt 780
aaagggcacg gtgggtgtat ctgcactaac aaactttott tatctaattt aaaaacgggtg 840
actctcacta aaaactctgc aaaggagctc ggaggagcta tttttacaga tctagcgtct 900
ataccacaaa cagatacccc agagtcttct accccctott cctctcgcgc tgaagcaact 960
cccgaaagtag ttgtctctgc taaaaataat cgattctttg cctctacggc agaaccggca 1020
gccctctctc taacagaggc tgagctctat caaacggatc aaacagaaac tctctgatact 1080
aatagcgata tagacgtgtc gattgagaac attttgaatg tgcgtatcaa tcaaaccaact 1140
tctgcgaaaa aaggaggggc tatttcaggg aaaaaagcta aactttcccg tattaaacaat 1200
cttgaacttt caggggaattc atcccaggat gtaggaggag gtctctgttt aactgaaagc 1260
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gggtttattc attctaaaac gggtactcta tctaactcta agtctacctt cacttttgca 1380
gataaacactg ttaaagcaat agtagaagc actcctgaag ctccagaaga gattcctcca 1440
gtagaaggag aagagtctac agcaacagaa aatccgaatt ctaatacaga aggaagtctg 1500
gctaacaacta accttgaagg atctcaaggg gatactgctg atacagggaac tgggtgttgt 1560
aacatactagt ctcaagacat atcagatact ggaaacgtg aatctggaga acaactacaa 1620
gattctcaac aatctaatag agaaaatacc cttcccaata gtagattga tcaacttaac 1680
gaaaacacag acgaatcctc tgatagccac actgaggaaa taactgacga gagtgtctca 1740
tcgtctctct aa 1752

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<210> 353

<211> 583

<212> PRT

<213> Chlamydia trachomatis

<400> 353

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Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1 5 10 15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
20 25 30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
35 40 45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
50 55 60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65 70 75 80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
85 90 95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
100 105 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
115 120 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
130 135 140
Arg Pro Leu Asp Thr Gln Val Ser Glu Ser Pro Glu Ser Thr Pro Ser
145 150 155 160
Pro Asp Asp Val Leu Gly Lys Gly Gly Ile Tyr Thr Glu Lys Ser
165 170 175
Leu Thr Ile Thr Gly Ile Thr Gly Thr Ile Asp Phe Val Ser Asn Ile
180 185 190
Ala Thr Asp Ser Gly Ala Gly Val Phe Thr Lys Glu Asn Leu Ser Cys
195 200 205
Thr Asn Thr Asn Ser Leu Gln Phe Leu Lys Asn Ser Ala Gly Gln His
210 215 220
Gly Gly Gly Ala Tyr Val Thr Gln Thr Met Ser Val Thr Asn Thr Thr
225 230 235 240

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[illegible]

<210> 354

<211> 39

<212> DNA

<213> Chlamydia trachomatis

<400> 354

gagagcggcc gctcgatcaa tctaacgaaa acacagacg

39

<210> 355

<211> 36

<212> DNA

<213> Chlamydia trachomatis

<400> 355
gagagcggcc gcttagacca aagctccatc agcaac 36

<210> 356
<211> 2052
<212> DNA
<213> *Chlamydia trachomatis*

<400> 356
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cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120
accgttcata tcgggacctac cgccttcttc ggcttgggtg ttgtcgacaa caacggcaac 180
ggcgacagag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
ggcgacgtga tcaccgcggt cgacggcgct cggatcaact cggccaccgc gatggcggac 300
gcgcttaaac ggcatactcc cgggtgacgt atctcggtga cctggcgaac caagtcgggc 360
ggcacgcgta caggggaacgt gacattggcc gagggaccoc cggccgaatt ctgcagatat 420
ccatcacact ggccggccgt cgatcaatct aacgaaaaca cagacgaatc atctgatagc 480
cacactgagg aaataactga cgagagtgtc tcatcgtcct ctaaaagtgg atcatctact 540
cctcaagatg gagggagcgc ttcttcaggg gctccctcag gagatcaatc tatctctgca 600
aacgcttggt tagctaaaag ctatgtctcg agtactgata gctccctcgt atctaattct 660
tcaggttccag acgttactgc atcttctgat aatccagact cttctctcgc tggagatagc 720
gctggagact ctgaaggacc gactgagcca gaagctgggt ctacaacaga aactcctact 780
ttaataggag gagggwctat ctatggagaa actgttaaga ttgagaactt cctcggccaa 840
ggaatatatt ctggaacaaa agctatcgat aacaccacag aaggctcctc ttccaaaatt 900
aacgctctcg gaggtgcggt ctatgctaaa acattgttta atctcgatag cgggagctct 960
agacgaactg tcactctctc cgggaataact gtctctctc aatctacaac aggtcaggtt 1020
gctggaggag ctatctactc tctactgtga accattgcta ctctgtgtat atttctctaa 1080
aactctgcaa caaaccaatgc taataacgct acagatactc agagaaaaga cacttttgga 1140
ggagctatcg gagctacttc tgcgttttct ctatcaggag gggctcattt tttagaaaac 1200
gttgctgacc tcggatctgc tattgggttg ttggcagaca cacaaaaaac agaaacagtg 1260
aaatagagtg ctggctccta ctactttgaa aaaaataaag ctttaaaacg agctactatt 1320
tacgcacctg tcgtttccat taaagcctat actgcacat ttaaccaaaa cagatctcta 1380
gaagaaggaa gcgcgattta ctttacaana gaagcactta ttgagtcttt aggtctctgt 1440
ctctttcacg gaaacttagt aaccccaacg ctaagcacia ctacagaagg cacaccagcc 1500
acaacctcag gagatgtaac aaaataggt gctgctactt ttggcaaat agcaagctca 1560
aacggatctc agacggataa ccttccctcg aaactcattg cttcaggagg aaatatttgt 1620
ttccgaacaa atgaataccg tctacttctc tctgataccg gaacctctac tttctgtagt 1680
attgcgggag atgtttaaatt aaccatgcga cgtcgaaaag ggaaaaacgat cagtttcttt 1740
gatgcaatcc ggacctctac taagaaaaca ggtacacagg caactgccta cgatactctc 1800
gatattaata aatctgagga ttcagaaaact gtaaacctg cgtttacagg aacgactctg 1860
gtattctctg aattacatga aataaaatcc tatattccac aaacagtagt tctacacagt 1920
ggatctcttg tattgaagcc aaataccagc cttcatgtca tttcttttga cgagaaagaa 1980
ggctcttctc tcgttatgac aactggatct tctctttcga accagactgt tgcgtaggtga 2040
gctttgggtct aa 2052

<210> 357
<211> 683
<212> PRT
<213> *Chlamydia trachomatis*

<400> 357
Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
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Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
20 25 30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
35 40 45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val

50	55	60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr		
65	70	75
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr		80
	85	90
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser		95
	100	105
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr		110
	115	120
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp		125
	130	135
Arg Pro Leu Asp Gln Ser Asn Glu Asn Thr Asp Glu Ser Ser Asp Ser		140
	145	150
His Thr Glu Glu Ile Thr Asp Glu Ser Val Ser Ser Ser Lys Ser		155
	160	165
Gly Ser Ser Thr Thr Gln Asp Gly Gly Ala Ala Ser Ser Gly Ala Pro		170
	175	180
Ser Gly Asp Gln Ser Ile Ser Ala Asn Ala Cys Leu Ala Lys Ser Tyr		185
	190	195
Ala Ala Ser Thr Asp Ser Ser Pro Val Ser Asn Ser Ser Gly Ser Asp		200
	205	210
Val Thr Ala Ser Ser Asp Asn Pro Asp Ser Ser Ser Gly Asp Ser		215
	220	225
Ala Gly Asp Ser Glu Gly Pro Thr Glu Pro Glu Ala Gly Ser Thr Thr		230
	235	240
Glu Thr Pro Thr Leu Ile Gly Gly Ala Ile Tyr Gly Glu Thr Val		245
	250	255
Lys Ile Glu Asn Phe Ser Gly Gln Gly Ile Phe Ser Gly Asn Lys Ala		260
	265	270
Ile Asp Asn Thr Thr Glu Gly Ser Ser Ser Lys Ser Asn Val Leu Gly		275
	280	285
Gly Ala Val Tyr Ala Lys Thr Leu Phe Asn Leu Asp Ser Gly Ser Ser		290
	295	300
Arg Arg Thr Val Thr Phe Ser Gly Asn Thr Val Ser Ser Gln Ser Thr		305
	310	315
Thr Gly Gln Val Ala Gly Gly Ala Ile Tyr Ser Pro Thr Val Thr Ile		320
	325	330
Ala Thr Pro Val Val Phe Ser Lys Asn Ser Ala Thr Asn Asn Ala Asn		335
	340	345
Asn Ala Thr Asp Thr Gln Arg Lys Asp Thr Phe Gly Gly Ala Ile Gly		350
	355	360
Ala Thr Ser Ala Val Ser Leu Ser Gly Gly Ala His Phe Leu Glu Asn		365
	370	375
Val Ala Asp Leu Gly Ser Ala Ile Gly Leu Val Pro Asp Thr Gln Asn		380
	385	390
Thr Glu Thr Val Lys Leu Glu Ser Gly Ser Tyr Tyr Phe Glu Lys Asn		395
	400	405
Lys Ala Leu Lys Arg Ala Thr Ile Tyr Ala Pro Val Val Ser Ile Lys		410
	415	420
Ala Tyr Thr Ala Thr Phe Asn Gln Asn Arg Ser Leu Glu Glu Gly Ser		425
	430	435
Ala Ile Tyr Phe Thr Lys Glu Ala Ser Ile Glu Ser Leu Gly Ser Val		440
	445	450
Leu Phe Thr Gly Asn Leu Val Thr Pro Thr Leu Ser Thr Thr Thr Glu		455
	460	465
Gly Thr Pro Ala Thr Thr Ser Gly Asp Val Thr Lys Tyr Gly Ala Ala		470
	475	480
Ile Phe Gly Gln Ile Ala Ser Ser Asn Gly Ser Gln Thr Asp Asn Leu		485
	490	495
	500	505
	510	

	515		520		525	
Pro	Leu	Lys	Leu	Ile	Ala	Ser
	530		535		540	
Glu	Tyr	Arg	Pro	Thr	Ser	Ser
545			550		555	
Ile	Ala	Gly	Asp	Val	Lys	Leu
			565		570	
Ile	Ser	Phe	Phe	Asp	Ala	Ile
			580		585	
Gln	Ala	Thr	Ala	Tyr	Asp	Thr
			595		600	
Glu	Thr	Val	Asn	Ser	Ala	Phe
			610		615	
Leu	His	Glu	Asn	Lys	Ser	Tyr
625					630	
Gly	Ser	Leu	Val	Leu	Lys	Pro
					645	
Glu	Gln	Lys	Glu	Gly	Ser	Ser
			660		665	
Ser	Asn	Gln	Thr	Val	Ala	Asp
			675		680	